

Tue Apr 20 12:43:37 2004

US-09-925-637-63.rn1

Page 1

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 07:00:11 ; Search time 94 Seconds
(without alignments)
5083.114 Million cell updates/sec

Title: US-09-925-637-63

Perfect score: 861 atgacgaatctaccgatgaa.....tattagaatcgttattta 861

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ins/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ins/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ins/5A_COMB.seq:*
4: /cgn2_6/ptodata/2/ins/5B_COMB.seq:*
5: /cgn2_6/ptodata/2/ins/5A_COMB.seq:*
6: /cgn2_6/ptodata/2/ins/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	861	100.0	1893	4 US-08-956-171E-155	Sequence 155, App
2	606	70.4	882	3 US-09-276-873-1	Sequence 1, Appl
3	25	2.9	909	4 US-09-134-001C-134	Sequence 334, App
C 4	19	2.2	640681	4 US-09-790-988-1	Sequence 1, Appl
5	18	2.1	753	4 US-09-484-970B-110	Sequence 110, App
6	18	2.1	1301	1 US-07-686-322A-1	Sequence 1, Appl
7	18	2.1	1301	1 US-08-002-899-1	Sequence 1, Appl
8	18	2.1	5163	3 US-08-700-651-1	Sequence 1, Appl
9	18	2.1	5163	3 US-08-928-361B-4	Sequence 1, Appl
10	18	2.1	5163	3 US-09-588-995A-4	Sequence 4, Appl
11	18	2.1	5318	3 US-08-700-651-2	Sequence 2, Appl
12	18	2.1	5318	3 US-08-928-361B-3	Sequence 3, Appl
13	18	2.1	5318	3 US-09-588-995A-3	Sequence 2, App
14	18	2.1	10146	4 US-08-956-171E-243	Sequence 243, App
15	18	2.1	786431	4 US-09-751-389-3	Sequence 3, Appl
C 16	18	2.1	786431	4 US-09-751-389-3	Sequence 3, Appl
17	17	2.0	540	4 US-09-702-705-1416	Sequence 1416, Ap
18	17	2.0	540	4 US-09-736-457-1416	Sequence 1416, Ap
19	17	2.0	540	4 US-09-614-124B-1416	Sequence 1416, Ap
20	17	2.0	540	4 US-09-671-325-1416	Sequence 1416, Ap
21	17	2.0	604	3 US-09-385-982-404	Sequence 404, App
22	17	2.0	616	3 US-09-385-982-173	Sequence 173, App
23	17	2.0	660	2 US-08-902-516-1	Sequence 1, Appl
24	17	2.0	660	2 US-09-847-185-1	Sequence 1, Appl
25	17	2.0	1132	4 US-09-203-958A-1	Sequence 1, Appl
26	17	2.0	1135	4 US-09-203-958A-3	Sequence 3, Appl
27	17	2.0	1164	4 US-09-134-001C-2199	Sequence 2199, Ap

28	17	2.0	1239	4 US-09-543-681A-4146	Sequence 4146, Ap
29	17	2.0	1511	2 US-08-809-763-3	Sequence 3, Appl
30	17	2.0	1511	3 US-08-956-253-3	Sequence 3, Appl
31	17	2.0	2335	2 US-08-300-584-3	Sequence 3, Appl
32	17	2.0	2335	3 US-08-476-123-3	Sequence 3, Appl
33	17	2.0	2517	4 US-09-328-352-3410	Sequence 3410, Ap
C 34	17	2.0	2517	4 US-09-371-338-20	Sequence 20, Appl
C 35	17	2.0	3374	4 US-09-205-258-184	Sequence 184, App
C 36	17	2.0	4666	3 US-09-150-460B-14	Sequence 4, Appl
C 37	17	2.0	6085	4 US-09-800-729-35	Sequence 35, Appl
C 38	17	2.0	6614	3 US-09-150-460B-3	Sequence 3, Appl
39	17	2.0	7258	4 US-09-058-483-8	Sequence 8, Appl
40	17	2.0	14561	4 US-09-392-714-1	Sequence 1, Appl
C 41	17	2.0	193303	4 US-09-497-855A-37	Sequence 37, Appl
C 42	17	2.0	193303	4 US-09-497-855A-44	Sequence 44, Appl
C 43	17	2.0	580073	4 US-08-545-528D-1	Sequence 1, Appl
C 44	17	2.0	1664976	4 US-08-916-421B-1	Sequence 1, Appl
C 45	17	2.0	4403765	3 US-09-103-840A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-956-171E-155/c
Sequence 155, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-08-956-171E-155

Tue Apr 20 12:43:37 2004

us-09-925-637-63.rn1

Page 2

Query Match 100.0%; Score 861; DB 4; Length 1893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTTGCG 60
DB 1314 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTTGCG 1255
QY 61 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 1254 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1195
QY 121 GGAGGTAAACGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
DB 1194 GGAGGTAAACGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 1135
QY 181 TATGATTAAGTATGAAGGCGAATGCACTAGAAATGATTCATTAATTCATTAATTCATTAAT 240
DB 1134 TATGATTAAGTATGAAGGCGAATGCACTAGAAATGATTCATTAATTCATTAATTCATTAAT 1075
QY 241 CATGATGACCTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 1074 CATGATGACCTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
QY 301 AAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 1014 AAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
QY 361 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 954 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
QY 421 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 894 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835
QY 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 834 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 775
QY 541 TTATTAATCTTTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 774 TTATTAATCTTTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715
QY 601 GAACATTTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 714 GAACATTTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
QY 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 654 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
QY 721 AATAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 594 AATAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
QY 781 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 534 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 474 TTATTAAGAAATCGTTGATTTA 454
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RESULT 2
US-09-276-873-1

; Sequence 1, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwin Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: Ispa

; FILE REFERENCE: GMI0208
; CURRENT APPLICATION NUMBER: US/09/276, 873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-276-873-1

Query Match 70.4%; Score 606; DB 3; Length 882;
Best Local Similarity 99.4%; Pred. No. 76-297;
Matches 856; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTTGCG 60
DB 1 ATGCGAATCTACCGATGATTAATTAATGATGAAGTCAATTAATGATTAATCGGTTGCG 60
QY 61 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 ATAAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 GGAGGTAAACGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
DB 121 GGAGGTAAACGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
QY 181 TATGATTAAGTATGAAGGCGAATGCACTAGAAATGATTCATTAATTCATTAATTCATTAAT 240
DB 181 TATGATTAAGTATGAAGGCGAATGCACTAGAAATGATTCATTAATTCATTAATTCATTAAT 240
QY 241 CATGATGACCTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 CATGATGACCTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 AAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 AAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 CTGTCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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DB 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TTATTAATCTTTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TTATTAATCTTTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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DB 601 GAACATTTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 AATAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 AATAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 CATAGAGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 841 TTATTAAGAAATCGTTGATTTA 861
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Db 841 TTATTAGAAATCGTTGATTTA 861

RESULT 3

US-09-134-001C-334
Sequence 334, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 334
LENGTH: 909
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-334

Query Match 2.9%; Score 25; DB 4; Length 909;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 GAGGAAATTAACAATCATTAAGT 305
308 GAGGAAATTAACAATCATTAAGT 332

RESULT 4

US-09-790-988-1/c
Sequence 1, Application US/09790988
Patent No. 6632935
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: MATSUDA, HIROMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHITAKA
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 2.2%; Score 19; DB 4; Length 640681;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 AATAAATTATAGATGAG 37
214082 AATAAATTATAGATGAG 214064

RESULT 5

US-09-484-970B-110
Sequence 110, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne

APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 110
LENGTH: 763
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 009051.5CB1
US-09-484-970B-110

Query Match 2.1%; Score 18; DB 4; Length 763;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GATGAAATTAATTAATGA 32
212 GATGAAATTAATTAATGA 229

RESULT 6

US-07-686-322A-1
Sequence 1, Application US/07686322A
Patent No. 5312733
GENERAL INFORMATION:
APPLICANT: MacLeod Dr., Carol L.
TITLE OF INVENTION: No. 5312733el T-cell lymphoma CDNA clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/686,322A
FILING DATE: 19910411
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/509684
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5232-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-3634
TELEFAX: (713) 651-5246
TELEX: Western Union 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: AKR1 Jackson
INDIVIDUAL ISOLATE: SL12 cell line
TISSUE TYPE: lymphoma
CELL TYPE: T-cell

Tue Apr 20 12:43:37 2004

us-09-925-637-63.rni

Page 4

CELL LINE: SL12.3 and SL12.4
IMMEDIATE SOURCE:
CLONE: 19.1
US-07-686-322A-1

Query Match 2.1%; Score 18; DB 1; Length 1301;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CCAATCAAAACCTTATT 845
DB 3 CCAATCAAAACCTTATT 20

RESULT 7
US-08-002-999-1
Sequence 1, Application US/08002999
Patent No. 5440017
GENERAL INFORMATION:
APPLICANT: Macleod Dr., Carol L.
TITLE OF INVENTION: No. 5440017el T-cell lymphoma CDNA clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,999
FILING DATE: 19930111
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,322
FILING DATE: 11-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D-5232-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-5587
TELEFAX: (713) 651-5246
TELEX: Western Union 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: AKR1 Jackson
INDIVIDUAL ISOLATE: SL12 cell line
TISSUE TYPE: Lymphoma
CELL LINE: T-cell
CELL LINE: SL12.3 and SL12.4
IMMEDIATE SOURCE:
CLONE: 19.1
US-08-002-999-1

Query Match 2.1%; Score 18; DB 1; Length 1301;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CCAATCAAAACCTTATT 845
DB 3 CCAATCAAAACCTTATT 20

DB 3 CCAATCAAAACCTTATT 20

RESULT 8
US-08-700-651-1
Sequence 1, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUY, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 5163
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-08-700-651-1

Query Match 2.1%; Score 18; DB 3; Length 5163;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATGATCTTGAACCT 507
DB 3769 CCAATGATCTTGAACCT 3786

RESULT 9
US-08-928-361B-4
Sequence 4, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VERNY, HANA
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677

TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5163 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-928-361B-4

Query Match 2.1%; Score 18; DB 3; Length 5163;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507
DB 3769 CCAATTGATCTTGAAGT 3786

RESULT 10
US-09-588-995A-4
Sequence 4, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 5163
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-09-588-995A-4

Query Match 2.1%; Score 18; DB 4; Length 5163;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507
DB 3769 CCAATTGATCTTGAAGT 3786

RESULT 11
US-08-700-651-2
Sequence 2, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LERCH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B

CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5318
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-08-700-651-2

Query Match 2.1%; Score 18; DB 3; Length 5318;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507
DB 3769 CCAATTGATCTTGAAGT 3786

RESULT 12
US-08-928-361B-3
Sequence 3, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-928-361B-3

Query Match 2.1%; Score 18; DB 3; Length 5318;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAAGT 507
DB 3769 CCAATTGATCTTGAAGT 3786

Tue Apr 20 12:43:37 2004

us-09-925-637-63.inl

Page 6

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RESULT 13
US-09-588-995A-3
Sequence 3, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUY, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 5318
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-09-588-995A-3

Query Match      2.1% Score 18; DB 4; Length 5318;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      490 CCAATTGATCTTGAACCT 507
Db      3769 CCAATTGATCTTGAACCT 3786

RESULT 14
US-08-956-171E-243
Sequence 243, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
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FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 10146 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 243:

US-08-956-171E-243

Query Match      2.1% Score 18; DB 4; Length 10146;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      319 ACTGCGATTTGACAGCT 336
Db      9771 ACTGCGATTTGACAGCT 9788

RESULT 15
US-09-751-389-3
Sequence 3, Application US/09751389
Patent No. 6630334
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: C1001067
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 786431
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(786431)
OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match      2.1% Score 18; DB 4; Length 786431;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      613 AGTTATAGTTATCATTTA 630
Db      3108 AGTTATAGTTATCATTTA 3125

Search completed: April 20, 2004, 08:09:37
Job time : 107 secs
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Tue Apr 20 12:43:37 2004

US-09-925-637-63.rnpb

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using BW model

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Perfect score: 861

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Gapop 60.0 , Gapext 60.0

Searched: 2890132 seqs, 2237290429 residues

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19: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	861	100.0	861	15	US-10-084-205-63
3	861	100.0	1893	8	US-08-781-866-155
4	861	100.0	1893	13	US-10-329-624-155
5	657	76.3	882	13	US-10-122A-122A-8179
6	489	56.8	882	9	US-09-815-242-8485
7	474	55.1	884	9	US-09-815-242-4184
8	413	48.0	413	9	US-09-815-242-2822
9	413	48.0	413	13	US-10-282-122A-5390
10	337	39.1	337	9	US-09-815-242-3275
11	337	39.1	337	13	US-10-282-122A-5841
12	25	2.9	879	13	US-10-282-122A-34531
13	21	2.4	885	13	US-10-282-122A-17062
14	21	2.4	891	16	US-10-369-493-40236

15	20	2.3	858	16	US-10-369-493-42078	Sequence 42078, A
16	20	2.3	879	13	US-10-282-122A-35068	Sequence 35068, A
17	20	2.3	918	16	US-10-369-493-33874	Sequence 33874, A
18	20	2.3	1023	13	US-10-425-114-7546	Sequence 7546, Ap
19	20	2.3	122859	13	US-10-087-192-37	Sequence 37, Appl
20	19	2.2	151	9	US-09-864-761-24950	Sequence 24950, A
21	19	2.2	580	13	US-10-027-632-194294	Sequence 194294, A
22	19	2.2	580	13	US-10-027-632-194295	Sequence 194295, A
23	19	2.2	580	16	US-10-027-632-194294	Sequence 194294, A
24	19	2.2	580	16	US-10-027-632-194295	Sequence 194295, A
25	19	2.2	600	9	US-09-864-761-8212	Sequence 8212, Ap
26	19	2.2	922	13	US-10-027-632-21738	Sequence 21738, A
27	19	2.2	922	13	US-10-027-632-21739	Sequence 21739, A
28	19	2.2	922	16	US-10-027-632-21738	Sequence 21738, A
29	19	2.2	922	16	US-10-027-632-21739	Sequence 21739, A
30	19	2.2	71887	13	US-10-087-192-1654	Sequence 1654, Ap
31	19	2.2	130427	15	US-10-175-522-87	Sequence 87, Appl
32	19	2.2	640681	9	US-09-790-988-1	Sequence 1, Appl
33	19	2.2	2940917	13	US-10-027-632-174763	Sequence 174763, A
34	19	2.2	2940917	16	US-10-027-632-174763	Sequence 174763, A
35	18	2.1	118	9	US-09-764-878-357	Sequence 357, App
36	18	2.1	118	15	US-10-079-854-357	Sequence 357, App
37	18	2.1	322	14	US-10-040-739-374	Sequence 374, App
38	18	2.1	449	9	US-09-983-965-3145	Sequence 3145, Ap
39	18	2.1	509	13	US-10-027-632-26964	Sequence 26964, A
40	18	2.1	509	16	US-10-027-632-26964	Sequence 26964, A
41	18	2.1	562	13	US-10-027-632-114822	Sequence 114822, A
42	18	2.1	562	16	US-10-027-632-114822	Sequence 114822, A
43	18	2.1	637	13	US-10-027-632-189412	Sequence 189412, A
44	18	2.1	637	13	US-10-027-632-189413	Sequence 189413, A
45	18	2.1	637	16	US-10-027-632-189412	Sequence 189412, A

ALIGNMENTS

RESULT 1
US-09-925-637-63
Sequence 63, Application US/09925637
Patent No. US2002010338A1
GENERAL INFORMATION:
APPLICANT: Chai
TITLE OR INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: P5560
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/151,933
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781,986
PRIOR FILING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-637-63
Query Match 100.0%; Score 861; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGACGATCTACCGATGAATTAATTAATAGATGAAGCAATTAATGATTCGTTGGC 60
QY 61 ATAAATTAATAGTAATGATGATCTACGATGAAGAAAGTATGTTGTAATTAATGCT 120

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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-084-205-63
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181 TATGAGTTAGGTATGAAGAGCGCAATTGCACTAGAAATGATTCATATTCATTATT 240
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RESULT 2
US-10-084-205-63
; Sequence 63, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, GJ1
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P8513P1
; CURRENT APPLICATION NUMBER: US/10/084, 205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 63

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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-084-205-63
Query Match 100.0%; Score 861; DB 15; Length 861;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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421 CTGTCATATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 480
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841 TTATTAAGAAATCGTTGATTTA 861

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RESULT 3
US-08-781-986A-155/c
; Sequence 155, Application US/08781986A

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; INFORMATION FOR SEQ ID NO: 155:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1893 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 155:
 US-10-329-624-155

Query Match 100.0%; Score 861; DB 13; Length 1893;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1254 ATAAATTAATCACTATGATGATCTAGCTAGAGAAAGTATGTTATCATTAATGCT 1195
QY 121 GGAGTAAACGATCCGACCGAGTCTGTATTAATCACTTTAGATTCACTAAATACCGAG 180
DB 1194 GGAGTAAACGATCCGACCGAGTCTGTATTAATCACTTTAGATTCACTAAATACCGAG 1135
QY 181 TATGAGTTAGGTATGAAGAGCGCAATTGCACTAGAAATGATTCATATCACTTAT 240
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QY 241 CATGATACCTACGACGATGATGATTAATGATGATTCATGACGAGAAATTAACAATCAT 300
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DB 1014 AAAGTATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
QY 361 GAAGTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 954 GAAGTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
QY 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 894 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835
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DB 594 AATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
QY 781 CATAGAGCGAGCGAGTGAATGAATCAAGCAATGATGATGATGATGATGATGATGATGAT 840
DB 534 CATAGAGCGAGCGAGTGAATGAATCAAGCAATGATGATGATGATGATGATGATGATGAT 475
QY 841 TTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
DB 474 TTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
  
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RESULT 5
 US-10-282-122A-8179
 ; Sequence 8179, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselebeck, Robert
 ; APPLICANT: Ohlsen, Karl
 ; APPLICANT: Zykkind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27,931
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8179
 ; LENGTH: 882
 ; TYPE: DNA
 ; ORGANISM: *Staphylococcus aureus*
 US-10-282-122A-8179

Query Match 76.3%; Score 657; DB 13; Length 882;
 Best Local Similarity 99.5%; Pred. No. 2,2e-314;
 Matches 857; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ATGACGAATCTACCGATGGAATAATTATAGATGAAGTCATATGAAATTATCGGTTGG 60
DB 1 ATGACGAATCTACCGATGGAATAATTATAGATGAAGTCATATGAAATTATCGGTTGG 60
QY 61 ATAAATTAATCACTATGATGATCTAGCTAGAGAAAGTATGTTATCATTAATGCT 120
DB 61 ATAAATTAATCACTATGATGATCTAGCTAGAGAAAGTATGTTATCATTAATGCT 120
QY 121 GGAGTAAACGATCCGACCGAGTCTGTATTAATCACTTTAGATTCACTAAATACCGAG 180
DB 121 GGAGTAAACGATCCGACCGAGTCTGTATTAATCACTTTAGATTCACTAAATACCGAG 180
QY 181 TATGAGTTAGGTATGAAGAGCGCAATTGCACTAGAAATGATTCATATCACTTAT 240
DB 181 TATGAGTTAGGTATGAAGAGCGCAATTGCACTAGAAATGATTCATATCACTTAT 240
QY 241 CATGATACCTACGACGATGATGATTAATGATGATGATGATGATGATGATGATGATGAT 300
  
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Db 241 CATGATGACCTACGACGCGATGATGATGATTAATGACGAGGAAAATTAAACAATCAT 300
Qy 301 AAAGTATATGGTGAAGTGAAGTGCATGATTAATGACGAGTGAAGTCTTATTAATTAAGCATTT 360
Db 301 AAAGTATATGGTGAAGTGAAGTGCATGATTAATGACGAGTGAAGTCTTATTAATTAAGCATTT 360
Qy 361 GAACCTATTTGACGATGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 420
Db 361 GAACCTATTTGACGATGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 420
Qy 421 CTGTCATAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
Db 421 CTGTCATAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
Qy 481 GAAGGCCAACCAATGATCTTGAAAATTGAAAATGATTAACCAAAACCAAAACCAAGAGCA 540
Db 481 GAAGGCCAACCAATGATCTTGAAAATTGAAAATGATTAACCAAAACCAAAACCAAGAGCA 540
Qy 541 TTATTAATCTTTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 TTATTAATCTTTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 601 GAACATTTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 GAACATTTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy 721 AATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 780
Db 721 AATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 780
Qy 781 CATAGAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Db 781 CATAGAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Qy 841 TTATTAAGAAATGCTGATTTA 861
Db 841 TTATTAAGAAATGCTGATTTA 861

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RESULT 6

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US-09-815-242-8485
Sequence 8485 Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22

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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8485
LENGTH: 882
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(882)
US-09-815-242-8485
Query Match 56.8%; Score 489; DB 9; Length 882;
Best Local Similarity 99.8%; Pred: No. 2.6e-231;
Matches 539; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGACGAATCTACCGATGATTAATTAATGATGAAGTCAATDAGATTAATGCGTTGCG 60
Db 1 ATGACGAATCTACCGATGATTAATTAATGATGAAGTCAATDAGATTAATGCGTTGCG 60
Qy 61 ATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 61 ATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Qy 121 GAAGTAAAGCAGTCCGACCAAGTCTGTTATTAATGATGATGATGATGATGATGATGATGATGAT 180
Db 121 GAAGTAAAGCAGTCCGACCAAGTCTGTTATTAATGATGATGATGATGATGATGATGATGATGAT 180
Qy 181 TATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
Db 181 TATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
Qy 241 CATAGAGCCTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 241 CATAGAGCCTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy 301 AAAGTATATGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360
Db 301 AAAGTATATGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360
Qy 361 GAACCTATTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 GAACCTATTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 CTGTCATAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
Db 421 CTGTCATAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
Qy 481 GAAGGCCAACCAATGATCTTGAAAATTGAAAATGATTAACCAAAACCAAAACCAAGAGCA 540
Db 481 GAAGGCCAACCAATGATCTTGAAAATTGAAAATGATTAACCAAAACCAAAACCAAGAGCA 540

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RESULT 7

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US-09-815-242-4184
Sequence 4184 Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078

```

```

; APPLICANT: Zyskind, Judith W.
;
; APPLICANT: Wall, Daniel
;
; APPLICANT: Trawick, John D.
;
; APPLICANT: Carr, Grant T.

```

APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith

Query March 1	39.1%;	Score 337;	DB 13.7;	Length 337;
Best Local Similarity	100.0%;	Pred. No. 3	8e-156;	
Matches 337;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

QY	225	TACATATTCACTTATTCATGATGACCTTACCAAGCATGATATATGATGATATATGACGAGG	284
Db	337	TACATATTCACTTATTCATGATGACCTTACCAAGCATGATATATGATGATATATGACGAGG	278
QY	285	AAATTTAACAAATCATTAAAGTATATGCTGATGAGACTCCGATATTAGCAGTATGCTTT	344
Db	277	AAATTTAACAAATCATTAAAGTATATGCTGATGAGACTCCGATATTAGCAGTATGCTTT	218
QY	345	ATTATCAAGAAAGCTTTGAACTTATTCAGAGTATGATGATTAATCTGATGAAGTAAAT	404
Db	217	ATTATCAAGAAAGCTTTGAACTTATTCAGAGTATGATGATTAATCTGATGAAGTAAAT	158
QY	405	AAAAGTCTCAACGGCTGTCATATGACAGTGGTCATGTTGAAATGTCGGCGCTCAAT	464
Db	157	AAAAGTCTCAACGGCTGTCATATGACAGTGGTCATGTTGAAATGTCGGCGCTCAAT	98
QY	465	GTTAGATATGCAAAAGCGAAAGCCCAACCAATTGATCTTGAACCTTTGGAATGATACCA	524
Db	97	GTTAGATATGCAAAAGCGAAAGCCCAACCAATTGATCTTGAACCTTTGGAATGATACCA	38
QY	525	AACAAAACAGAGCACTTATTAACCTTTGGCTTATG	561
Db	37	AACAAAACAGAGCACTTATTAACCTTTGGCTTATG	1

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; SEQ ID NO 34531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34531

Query Match      2.9%; Score 25; DB 13; Length 879;
Beet Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      281 GAGGAAATTCACAATCATTAAGT 305
      |||||||
Db      281 GAGGAAATTACAAATCATTAAGT 305

RESULT 13
US-10-282-122A-17062
; Sequence 17062, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

```

```

; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 17062
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Clostridium difficile
US-10-282-122A-17062

Query Match          2.4%; Score 21; DB 13; Length 885;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 291 AACAAATCATTAAGTATATGG 311
    |||||
Db 297 AACAAATCATTAAGTATATGG 317

RESULT 14
US-10-369-493-40236
; Sequence 40236, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 40236
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-369-493-40236

Query Match          2.4%; Score 21; DB 16; Length 891;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Cy 214 GAATGATTCATCATATTC 234
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Db 226 GAATGATTCATCATATTC 246

RESULT 15
US-10-369-493-42078
; Sequence 42078, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 42078
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Lactococcus lactis
US-10-369-493-42078

Query Match          2.3%; Score 20; DB 16; Length 858;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 259 ATGATATATGATGATATATCG 278
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Db 247 ATGATATATGATGATATATCG 266

Search completed: April 20, 2004, 11:24:08
Job time : 369 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 05:55:16 / Search time 92 Seconds
(without alignments)
5193.617 Million cell updates/sec

Title: US-09-925-637-63

Perfect score: 861

Sequence: 1 atgacgaatcctacgcgatga.....tattagaatcgtgatcta 861

Scoring table: IDENTITY NUC
Gapex 10.0, Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCUTS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	861	100.0	1893	4	US-08-956-171E-155
2	853	99.1	882	3	US-09-276-873-1
3	449.8	52.2	909	4	US-09-134-001C-334
4	160.4	18.6	939	4	US-09-107-512A-3070
5	157.2	18.3	894	1	US-08-534-910B-5
6	155.6	18.1	893	1	US-08-333-321-1
7	155.6	18.1	894	1	US-08-534-910B-2
8	155.6	18.1	894	1	US-08-534-910B-3
9	155.6	18.1	894	1	US-08-534-910B-4
10	155.6	18.1	894	3	US-08-886-466-1
11	155.6	18.1	894	3	US-09-475-304-1
12	155.6	18.1	894	4	US-09-101-126-4
13	155.6	18.1	894	4	US-09-367-528A-4
14	154	17.9	894	1	US-08-534-910B-1
15	154	17.9	894	4	US-09-367-528A-2
16	150.6	17.5	486	4	US-09-217-609A-28
17	150.6	17.5	486	4	US-08-873-235B-28
18	141	16.4	924	4	US-09-543-681A-1736
19	137	15.9	1664976	4	US-08-916-421B-1
20	136.4	15.8	885	3	US-09-187-050-11
21	134.8	15.7	1179	3	US-09-187-050-13
22	134.8	15.7	1179	3	US-09-187-050-15
23	134.8	15.7	1179	3	US-09-187-050-17
24	134.8	15.7	1179	3	US-09-187-050-19
25	134.8	15.7	1179	3	US-09-187-050-21
26	134.8	15.7	1179	3	US-09-187-050-23
27	134.8	15.7	1179	3	US-09-187-050-25

28	134.8	15.7	1889	3	US-09-187-050-1	Sequence 1, Appl
29	134.4	15.6	847	4	US-09-634-238-85	Sequence 85, Appl
30	131.4	15.3	1830121	4	US-09-557-884-1	Sequence 1, Appl
31	131.4	15.3	1830121	4	US-09-643-990A-1	Sequence 1, Appl
32	124.6	14.5	876	3	US-09-275-742-1	Sequence 1, Appl
33	124.2	14.4	10011	4	US-08-961-527-76	Sequence 76, Appl
34	117.8	13.7	1029	4	US-09-540-236-692	Sequence 692, App
35	117.8	13.7	96109	4	US-09-596-002-35	Sequence 35, Appl
36	114.8	13.3	1914	4	US-09-634-238-41	Sequence 41, Appl
37	114.2	13.3	640681	4	US-09-790-988-1	Sequence 1, Appl
38	98.6	11.5	881	4	US-09-834-903-13	Sequence 13, Appl
39	92.4	10.7	927	4	US-09-328-352-64	Sequence 64, Appl
40	88.6	10.3	884	4	US-08-956-171E-185	Sequence 185, App
41	76.8	8.9	1284	4	US-08-858-207A-173	Sequence 173, App
42	72.6	8.4	861	3	US-09-187-050-4	Sequence 4, Appl
43	72	8.4	909	1	US-07-783-705A-7	Sequence 7, Appl
44	72	8.4	6918	1	US-07-783-705A-13	Sequence 13, Appl
45	71.4	8.3	990	1	US-08-410-167A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-956-171E-155/c
Sequence 155, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956, 171E
FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-08-956-171E-155


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Matches 856; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY	1	TTGAGCGAATCACCGGATGAATTAATTAATTAATGATGAATGCAATAATGAAATATCGGTTGCG	60
Db	1	ATGACGAATCTACCGATGAATTAATTAATTAATGATGAATGCAATAATGAAATATCGGTTGCG	60
QY	61	ATAAATAAATCAATATGATGACTCTACGCTTGAGAGAAAAGTATGTTGATTTCACTTAAACCT	120
Db	61	ATAAATAAATCAATATGATGACTCTACGCTCTGAAAGAAAAGCAAGTGTGATTTCACTTAAATCT	120
QY	121	GGAGGTAAAGCATCCGACCGAGTCTGTGTTATTTCACTTGTAGATTCTCTAATAACCGAG	180
Db	121	GGAGGTAAAGCATCCGACCGAGTCTGTGTTATTTCACTTGTAGATTCTCTAATAACCGAG	180
QY	181	TATGAGTTAGGTATGAAAGAGCGCAATTGCACTAAGAAATGATTCATACATATTCACCTTAT	240
Db	181	TATGAGTTAGGTATGAAAGAGCGCAATTGCACTAAGAAATGATTCATACATATTCACCTTAT	240
QY	241	CATGATGACCTACCGACGCGATGGAATATGATGATTATCGACGAGGAAAATTACAAATCAT	300
Db	241	CATGATGACCTACCGACGCGATGGAATATGATGATTATCGACGAGGAAAATTACAAATCAT	300
QY	301	AAAGTATTTGGTGAATGGAACCTGCATATTTACACAGTGTGCTTTATTAACCTAAAGCATTT	360
Db	301	AAAGTATTTGGTGAATGGAACCTGCATATTTACACAGTGTGCTTTATTAACCTAAAGCATTT	360
QY	361	GAACTTATTTCAAGTATGATAGATATTAATCTGATGAAATGTAATTAAGTTCTACACGG	420
Db	361	GAACTTATTTCAAGTATGATAGATATTAATCTGATGAAATGTAATTAAGTTCTACACGG	420
QY	421	CTGTCAATAGCAAGTGTCAATGTTGGAAATGTCGGCGGCTCAAAATGTTAGATATGCAAAAGC	480
Db	421	CTGTCAATAGCAAGTGTCAATGTTGGAAATGTCGGCGGCTCAAAATGTTAGATATGCAAAAGC	480
QY	481	GAAAGCCCAACCAATGATCTTGAAACTTTGAAATGATACACAAAACAAAAACAGAGCA	540
Db	481	GAAAGCCCAACCAATGATCTTGAAACTTTGAAATGATACACAAAACAAAAACAGAGCA	540
QY	541	TTATTAACCTTTGCGGTATGAGTGCACAGATATCGCTAAATGTCGATGATACAACTAAA	600
Db	541	TTATTAACCTTTGCGGTATGAGTGCACAGATATCGCTAAATGTCGATGATACAACTAAA	600
QY	601	GAAACATTTAGAAAGTTATAGTTATCATTTAGATATGATTCCTCAATTAABATGATTTA	660
Db	601	GAAACATTTAGAAAGTTATAGTTATCATTTAGATATGATTCCTCAATTAABATGATTTA	660
QY	661	TTAGACTGTATGATGATGAAGCAAGTTAGGTAATAAAAGTGGGCAAGCATTTGAAAT	720
Db	661	TTAGACTGTATGATGATGAAGCAAGTTAGGTAATAAAAGTGGGCAAGCATTTGAAAT	720
QY	721	AATAAAGTACGTACGTAGCTTATTAAGGAAAGATGGCGCAAGATTAATTTGACTAT	780
Db	721	AATAAAGTACGTACGTAGCTTATTAAGGAAAGATGGCGCAAGATTAATTTGACTAT	780
QY	781	CATAGAGACGACGAGCTGATGAATTAACGCAATTTGATGAACAAATTCATACAAACAC	840
Db	781	CATAGAGACGACGAGCTGATGAATTAACGCAATTTGATGAACAAATTCATACAAACAC	840
QY	841	TTATTAAGAAATGCTGATTTA	861


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QY 29 TAGATGAAGTCAATAATTAATTCGGTTCGATTAATAATCAATATGATCTCAGC 88
DB 80 TACCTGCTGAGAAAAGAAATCTTGTCTTTTATATAGATACAAAGGATTAAGGAC 139
QY 89 TAGAAGAAGTATGTTGATCTATCAATAAGCTGGAGAGTAAAGCATCGACAGTTCTGT 148
DB 140 TCTATATGCGAAGAGTATTCAGTGAAGACGCGGAGAAAGAAATACCTCTTATAC 199
QY 149 TATTACTCACTTATGATCTCAATAATACGAGTATGATT--AGGTATGAAGAGCGCA 205
DB 200 TTTTACGCGCGTTCCTTCTTATGATGAGCCTATGATGTCCTCCGCTATCAAGTACG 259
QY 206 TTGACACTGAAGATGATTCATACATATTCCTTTATCATGATGCTTACGAGGATGAGA 265
DB 260 CTGCTTTAGAAATGGTGCATACATATTCCTTATCCACATGATTTGCTGCGATGAGA 319
QY 266 ATGATGATATTCGACGAGAAATTAACAATATCAATATGATGATGATGAGTGCAG 325
DB 320 ATGATGATCTTCGAGAGAAAACCTACCATATTAAGATTCGCGAGAGATTAAGCTA 379
QY 326 TATTAGCAGTATGCTTTATTAATCAATGATTTGAATTTAATTTCAAGTATGATAT 385
DB 380 TATTGCGCGAGATGTTGCTTACAGAGCATTTCCAGCTAAT--CAGTATGGCACACT 436
QY 386 TAACTGATGAAGTAAATAAAGTCTTACAGCGGCTGCAATAGCAAGTGCATGTTG 445
DB 437 TAGGTAATTCCTCTAGAGCTTCTGCTCTTCAAGCATTAAGTCTGTTGGGAGATCAAG 496
QY 446 GAATGCTCGCGGCTCAATGTTAGATATGCAAAAGGAGCCACCAATTTGATCTTGA 505
DB 497 GTATGCTGCGGCAAGCTGCAATATCGAGGCGCATGAAAAGCTTCTTTAGAG 556
QY 506 CTTTGAAGATGATCAAAAAGCAAAACAGAGCATTTAATCTTTGGGATATAGTG 565
DB 557 AATTAGATTTATTCAGAAAAGAGAGAGGAGCTTTGATTCGTTATGCTTCTGCTG 616
QY 566 CAGCAGATATCGCTAATGCTGATGATCAATTAAGAACTTTAGAAAGTTATAGTTAT 625
DB 617 GTGCAATATTAAGCAACACCTGAGAAATCTTATGCTACTCAACGATTCAGCCGAA 676
QY 626 ATTTAGATGATGTTCCAGATTTAAAGATTTATTAAGCTGCTATGATGAGAGCA 685
DB 677 AATTAGATTTAGCTTTTCAAGTATGAGATATCTACGATGATGATGATGATGAT 736
QY 686 AGTAGGTAAGAAAGTGGGAGCGATCTGAAATAATAAAGTACGATGATGATTTAT 745
DB 737 CATTAGGGAAGAGCTGCTGATTAAGATGACGATGAGAAAATAATCTTACCCGCTTAT 796
QY 746 TAGGGAAGA 755
DB 797 TAGGCTTGA 806

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RESULT 5
US-08-534-910B-5

Sequence 5, Application US/08534910B
Patent No. 576911

GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi

APPLICANT: OBATA, Shunsei

APPLICANT: NISHINO, Tokuzo

APPLICANT: OHNUMA, Shinichi

APPLICANT: NAKAZAWA, Takeshi

APPLICANT: OGURA, Kyoze

APPLICANT: KOYAMA, Tanetoshi

TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable

TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W., Suite 600

CITY: Washington

```

STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534, 910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toifeneck, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-5

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Query Match 18.3%; Score 157.2; DB 1; Length 894;
Best Local Similarity 51.0%; Pred. No. 1.3e-29;
Matches 400; Conservative 0; Mismatches 378; Indels 6; Gaps 1;

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QY 17 TGAATTAATTAATGATTAATCAATTAATGATGATGATGATGATTAATTAATCAATTA 76
DB 29 TCAAGCAACAAAACAGCGGTGGAACAGCGCTCTCCGTTATATAGAGCGCTTAGAG 88
QY 77 TGGATCTCACTGAGAAAGATATGTTGATTTCAATTAATGATGATGATGATGATGAT 136
DB 89 GCGCGCGAAGGTAAAGAGAGATGCGTACTGATGAGAGCGCGCAACGAAATCC 148
QY 137 GACGATTTCTGTTATTAATCACTTATGATTAATTAATCAATTAATGATGATGAT 196
DB 149 GTCCCTGCTGCTTCTGCTCAACCGTTCAGGCGCTGCGAAAGACCGGCGATTCG 208
QY 197 AGAGCGCAATTCAGTAAATGATTCATACATATTCATTTATCATGATGATGATGAT 256
DB 209 CCGTGCCTGCGCGCATTAATGATCAATGATGATGATGATGATGATGATGATGAT 268
QY 257 CGATGATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 316
DB 269 GCATGAGCAACGATGATTTGCGCGCGCAAGCCGACGACGACGATTAAGTTCGCGAG 328
QY 317 GACATGCGATTAATTAAGTATGATGATGATGATGATGATGATGATGATGATGAT 371
DB 389 TCGACGATGAGCGCATTCCTCTCCGCTTCGCTTCGCTCATCGACGCGCTGCGAAG 448
QY 372 -AAGTATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 430
DB 389 TCGACGATGAGCGCATTCCTCTCCGCTTCGCTTCGCTCATCGACGCGCTGCGAAG 448
QY 431 CAAGGCTCATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 490
DB 449 CGCGCGCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
QY 491 CAATGATCTTGAACCTTTGAATGATTAACAAACAAACAAACAAACAGAGCATTTA 550
DB 509 CGCTGACGCTTCGAGCTGATATATTCATTCGCGCATTAACCGGGAATGCTGCAAT 568

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QY 551 TTGCGGTATGAGTGCAGAGATATGCTAATGTGATGATACAACTAAGAATCTTTAG 610
 Db 569 ACAGCGTGCACCGCGCCCTTGATGCGCGCTGATGCGCGCAAAACGCGGAGCTTG 628
 QY 611 AAGATATAGTTATCATTTAGGTATGATGTTCCAGATTAAGATGATTTAGACTGCT 670
 Db 629 ACGAATTCGCCCGCATCTAGGCTTGCTTCAATTCGCAATGATATTCGATTTG 688
 QY 671 ATGCTGATGAAGCAAGTTAGTTAAAAAGTGGCGACGATCTTGAATAATAAAGTA 730
 Db 689 AAGGGCAGAAAGAAAATCGCAAGCGGTGCGCAGCAGCAAAAGCAAAAGCGA 748
 QY 731 CGTACGTGAGTTATTAGGAAAGATGCGCGCAAGATTAATGACTTATCTAGAGAG 790
 Db 749 CGTATCCAGCGTTGCTGCTTGCGCGCGCAAGAAAGTTGGCGTTCATATCGAGG 808
 QY 791 CAGC 794
 Db 809 CGGC 812

RESULT 6

US-08-333-321-1
 / Sequence 1, Application US/0833321
 / Patent No. 5786192

GENERAL INFORMATION:

APPLICANT: Obata, Shushei
 TITLE OF INVENTION: FARNESYL PYROPHOSPHATE SYNTHETASE
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward W. Greason, Esq.
 STREET: 1 Broadway

CITY: New York

STATE: N.Y.

COUNTRY: U.S.A.

ZIP: 10004

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: NO.5786192epad, Windows 3.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,321

FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/953,424

FILING DATE: 29-SEP-1992

APPLICATION NUMBER: JP 3-253788

FILING DATE: 01-OCT-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Greason, Edward W.

REGISTRATION NUMBER: 18,918

REFERENCE/DOCKET NUMBER: 077670/00310

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 425-7200

TELEFAX: (212) 425-5288

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

LENGTH: 893 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Bacillus stearothermophilus
 US-08-333-321-1

Query Match 18.1%; Score 155.6; DB 1; Length 893;
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATTAATTAATGATGAAAGTCAATATGATATGCTGCGATTAATTAATCAAGTAA 76

Db 29 TCAACGACAAAACAGCGGTGAAAACAGCGCTCCCGTTATATAGACGGCTTAAG 88
 QY 77 TGAATCACTAGTAAAGAAATATGTTGTTATTCATTTAAATGCTGAGGTAAACGATCC 136
 Db 89 GGGCGGAGAACTGAAAAGCCGATGGCTATCATATGAGGCGCGGCAAGCAATCC 148
 QY 137 GACCAATTCCTGTTATTAATCACTTTAGATTCACTAAATACGATATGATGATGATGA 196
 Db 149 GTCCGTGCTGCTTCTCTCCACCGTTGCGGCGCTCGCAAGACCCGCGCTCGATTGC 208
 QY 197 AGAGCGAATTCACATGAATATGTTGATCATATTCATTTATGATGATGATGATGATGAT 256
 Db 209 CCGTCCGCTGCGGATGAAATGATTCATATGATGATGATGATGATGATGATGATGATGAT 268
 QY 257 CGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316
 Db 269 GCATGACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 328
 QY 317 GACTGCGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
 Db 329 CGATGCGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 388
 QY 372 -AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
 Db 389 TCGACGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 448
 QY 431 CAATGCTCATGTTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
 Db 449 CGCGCGGTCGGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
 QY 491 CAATGATCTTGAACCTTTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 550
 Db 509 CGCTGACGCTTTGGAAGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 568
 QY 551 TTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
 Db 569 ACAGGTGACACCGCGCGCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
 QY 611 AAGATTAATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 670
 Db 629 ACGAATTCGCCCGCATCTAGGCTTGCTTCAATTCGCAATGATATTCGATTTG 688
 QY 671 ATGCTGATGAAGCAAGTTAGTTAAAAAGTGGCGACGATCTTGAATAATAAAGTA 730
 Db 689 AAGGGCAGAAAGAAAATCGCAAGCGGTGCGCAGCAGCAAAAGCAAAAGCGA 748
 QY 731 CGTACGTGAGTTATTAGGAAAGATGCGCGCAAGATTAATGACTTATCTAGAGAG 790
 Db 749 CGTATCCAGCGTTGCTGCTTGCGCGCGCAAGAAAGTTGGCGTTCATATCGAGG 808
 QY 791 CAGC 794
 Db 809 CGGC 812

RESULT 7

US-08-534-910B-2
 / Sequence 2, Application US/08534910B
 / Patent No. 5766911

GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi
 APPLICANT: OBATA, Shushei

APPLICANT: NISHINO, Tokuzo

APPLICANT: OHNUMA, Shinichi

APPLICANT: NAKAZAWA, Takeshi

APPLICANT: OGURA, Kyoza

APPLICANT: KOYAMA, Tanetoshi

TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
 TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding The
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.
 ZIP: 20036-5405
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.25" Floppy Disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
 SOFTWARE: IBM/Word Perfect 6.1 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/534,910B
 FILING DATE: 28-SEPT-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-25253
 FILING DATE: 14-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Toffenetti, Judith L.
 REGISTRATION NUMBER: 39,048
 REFERENCE/DOCKET NUMBER: 77670/398
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)429-1776
 TELEFAX: (202)429-0796
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 ORIGINAL SOURCE:
 ORGANISM: Bacillus stearothermophilus
 US-08-534-910B-2

Query Match 18.1%; Score 155.6; DB 1; Length 894;
 Best Local Similarity 50.9%; Pired. No. 3.2e-29;
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATAATATATAGATGAAGTCAATATATATCGTGGATTAATAATCACTAA 76
 29 TCAACGACGCAAAACGCGGTGGAACACGCGTCCCGTTATAGACCGTTGAAG 88
 77 TGAATACCTAGCTAGAAAGAAAGTATGTTTATTCATTAAATGCTGAGGTTAA 136
 89 GGGCGGCGAAGGTGAAGAAAGCGATGCGTACTCATTTGAGCGCGGCAACGATCC 148
 137 GACCAAGTTCGTATTACTGACTTTAGATTCACTAAATCCGAGTATGATTAGTATA 196
 149 GTCCGTTGCTGCTTCTGTCCACCGTTCAGCGCTCGCAAGACCGCGCGTGGATTTC 208
 197 AGAGCGCAATGCACTGAAGATGATTATCATATTCATCTATTATTCATGACCTAC 256
 209 CCGTCCGCTCGCGATGGAATGATCCATGACTCTTTGATCCATGATGATTTGCCGA 268
 257 CGATGATATGATGATATGACGAGGAATTAACAATCAATAAGATATGAGAT 316
 269 GCAATGACACGATGATTTGCGGCGGCGAAGCCGACCAACCAATAGTTCGCGAGG 328
 317 GGAAGTGGATATAGCAGGTGATGCTTTATTAATCAAGCATTTGAATTTTC----- 371
 329 CGATGGCATCTGGGGGGGAGCGGTGTTGACGATCGGTTCAATTGATACCGAATA 388
 372 -AAGTATGATGATTTAATCTGATGAGTAAATAAAGTTCACAAACGCGCTCAATAG 430
 389 TCACAGATGAGCGATCCCTTCCTCCGCTCGGCTTCGCTCATCGAACGCTGCGAAG 448
 431 CAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490
 449 CGGCGGCTCGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
 491 CAATGATCTTGAACCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 550

509 CGCTGACCGCTTTCGAGCTGCAATATCAATTCATCGGCAATAAAACCGGAAAAATGCTGCAT 568
 551 TTGCGGTATAGATGACAGCAATATTCGCTAATGATGATGATGATGATGATGATGATG 610
 569 ACAGGTGACAGCGCGCTTATGATGCGCGCGCTGATGCGCGCAACCGGAGCGCTTG 628
 611 AAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 670
 629 ACGAATGCGCGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 688
 671 ATGCTGATGACAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 730
 689 AAGGCGAG 748
 731 CGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
 749 CGTATCAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
 791 CAGC 794
 809 CGGC 812

RESULT 8
 US-08-534-910B-3
 Sequence 3, Application US/08534910B
 Patent No. 5766911
 GENERAL INFORMATION:
 APPLICANT: KOIKE, Ayumi
 APPLICANT: OBATA, Shusei
 APPLICANT: NISHINO, Tokuzo
 APPLICANT: OHNUMA, Shinichi
 APPLICANT: NAKAZAWA, Takeshi
 APPLICANT: OGURA, Kyoza
 APPLICANT: KOYAMA, Taneoshi
 TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable
 TITLE OF INVENTION: Of Synthesizing Geranylgeranyl-diphosphate And Gene Coding The
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenyon & Kenyon
 STREET: 1025 Connecticut Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.
 ZIP: 20036-5405
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.25" Floppy Disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
 SOFTWARE: IBM/Word Perfect 6.1 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/534,910B
 FILING DATE: 28-SEPT-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-25253
 FILING DATE: 14-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Toffenetti, Judith L.
 REGISTRATION NUMBER: 39,048
 REFERENCE/DOCKET NUMBER: 77670/398
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)429-1776
 TELEFAX: (202)429-0796
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 ORIGINAL SOURCE:
 ORGANISM: Bacillus stearothermophilus

US-08-534-910B-3

Query Match 18.1%; Score 155.6; DB 1; Length 894;
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGATTGATTAATTAATCAATGA 76
 29 TCAACGAGAAAACAGCGGTGAAACGCGCTCTCCGTTATTAAGCGCTTAGAG 88
 77 TGAATCTCAGCTAGAGAAAGTATGTTGATTCATTAATAGCTGAGGTAAACGATCC 136
 89 GGCCTGCGAAGCTGAAAAAGCGATGGCTACTCATTTGAGGCGCGGCAAAACGAAATCC 148
 137 GACCACTTCTTATTAATCACTTAATGATCACTAAATACGAGATAGATGATGA 196
 149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTGAAAAAGACCGCGGCTGATTGC 208
 197 AGAGCGCAATTCACATAGAAATGATTCATACATATTCATTAATGATGACCTACGAG 256
 209 CCGTGCCTGCGCGATTAATGATTCATAGCTACTCTTTGATCATGATGATTTGCCGA 268
 257 CGATGATTAATGATTAATTCGACGAGAAAATTAACAATATTAAGTATATGTTGCT 316
 269 GATGAGACACATGATTTGCGCGCGCGGCAACCGACGAAACATTAAGTTGCGGAGG 328
 317 GCACTGCGATTTAGACAGGTGATGCTTTATTAATTAAGCATTTGAATTTTC----- 371
 329 CGATGCGCATCTTGGCGGGGAGCGGGTTGTTGACGTAGCGTTCAATTGATCAACGAAA 388
 372 -AAGTATATGATTAATCTGATGAAGTAAAAATTAAGTTTACAAAGCTGTCAATAG 430
 389 TCGACGATAGCGATCCCTCTCTCCGCTTCGCGCTCATCGAAGCGCTGGGGAAG 448
 431 CAAGTGTGATGTTGATGATGTCGCGGGTCAAAATGTTAGTATGCAAGCGAGCCAGC 490
 449 CGGCGGCTCGGAAGGATGCGCGCGCTGACGAGCGCATATGGAAGAGGAGGAAA 508
 491 CAATTGATCTGAAACTTTGAAATGATACAAAAAAGAGAGAGCTTATTAATT 550
 509 CCTGACGCTTCGAGAGCTCGAATCATTCATCGGTATTAACCGGAAAAATGCTGCAAT 568
 551 TTGCGGTTATGATGTCAGAGATATCGGTAAATGATGATGATCACTAAAGACTTTAG 610
 569 AAGAGGTGACAGCGCGCGCTTATGCGCGGCTGATGCGCGGCAACCGCGGAGCTTG 628
 611 AAGTTATAGTTATCATTTAGTATGATGATTCAGATTAAAGATTTATTAAGCTGCT 670
 629 ACGAATTCGCGCGCATCTAGGCTTGCCTTTCAAAATTCGCGATATATTCGATATG 688
 671 ATGTGATTAAGCAAAAGTTAGTAAAAAGTGGGCAAGGATCTTAAAAATTAATAATA 730
 689 AAGGGGCAAAAGAAAAATCGGCAAGCGGTCGAGGAGCAACAAAGCAAAAGGGA 748
 731 CGTACGTAGTTTATTAAGGAAAGATGGGCGAGAGATTAATGACTATCATAGAGAG 790
 749 CGATTCAGCGCTTGTCTGCTTGCCTGCGGCAAGGAAAGTTGCGCTTCATATCGAG 808

QY 791 CAGC 794
 DB 809 CGCG 812

RESULT 9
 US-08-534-910B-4
 ; Sequence 4; Application US/08534910B
 ; Patent No. 5766911
 ; GENERAL INFORMATION:
 ; APPLICANT: KOIKE, Ayumi
 ; APPLICANT: OABAT, Shusei
 ; APPLICANT: NISHINO, Tokuzo
 ; APPLICANT: OHNUMA, Shintchi
 ; APPLICANT: MAKIZAWA, Takeshi

APPLICANT: OGURA, Kyoze
 APPLICANT: KOYAMA, Taneosshi
 TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable
 TITLE OF INVENTION: Of Synthesizing Geranylgeranylphosphate And Gene Coding The
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenyon & Kenyon
 STREET: 1025 Connecticut Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.
 ZIP: 20036-5405
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.25" Floppy Disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
 SOFTWARE: IBM/Word Perfect 6.1 Windows
 CURRENT APPLICATION DATA:
 FILING DATE: 28-SEPT-1995
 CLASSIFICATION: 435
 APPLICATION NUMBER: US/08/534,910B
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-25253
 FILING DATE: 14-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Toftemetti, Judith L.
 REGISTRATION NUMBER: 39,048
 REFERENCE/DOCKET NUMBER: 77670/398
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)428-1776
 TELEFAX: (202)428-0796
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 ORIGINAL SOURCE:
 ORGANISM: Bacillus stearothermophilus
 US-08-534-910B-4

Query Match 18.1%; Score 155.6; DB 1; Length 894;
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGATTGATTAATTAATCAATGA 76
 29 TCAACGAGAAAACAGCGGTGAAACGCGCTCTCCGTTATTAAGCGCTTAGAG 88
 77 TGAATCTCAGCTAGAGAAAGTATGTTGATTCATTAATAGCTGAGGTAAACGATCC 136
 89 GGCCTGCGAAGCTGAAAAAGCGATGGCTACTCATTTGAGGCGCGGCAAAACGAAATCC 148
 137 GACCACTTCTTATTAATCACTTAATGATCACTAAATACGAGATAGATGATGA 196
 149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTGAAAAAGACCGCGGCTGATTGC 208
 197 AGAGCGCAATTCACATAGAAATGATTCATACATATTCATTAATGATGACCTACGAG 256
 209 CCGTGCCTGCGCGATTAATGATTCATAGCTACTCTTTGATCATGATGATTTGCCGA 268
 257 CGATGATTAATGATTAATTCGACGAGAAAATTAACAATATTAAGTATATGTTGCT 316
 269 GATGAGACACATGATTTGCGCGCGCGGCAACCGACGAAACATTAAGTTGCGGAGG 328
 317 GCACTGCGATTTAGACAGGTGATGCTTTATTAATTAAGCATTTGAATTTTC----- 371
 329 CGATGCGCATCTTGGCGGGGAGCGGGTTGTTGACGTAGCGTTCAATTGATCAACGAAA 388
 372 -AAGTATATGATTAATCTGATGAAGTAAAAATTAAGTTTACAAAGCTGTCAATAG 430
 389 TCGACGATAGCGCATCCCTCTCTCCGCTTCGCGCTCATCGAAGCGCTGGGGAAG 448

QY	43	CAAGTGGTCAATGTTGGAAATGATGCGGGGTCCAATGTAGATATGCAAAAGCGAAGGCCAAC	490
Db	449	CGGCGCGGTCCGGAAAGGAGATGTGCGCGGTCTACGAGCCCGAATATGTGAAAGAGAGGGGAAAA	508
QY	491	CAATTGATCTTGGAACTTTGGAAATGATACACAAAACAAAAACGAGACATTATTTAACTT	550
Db	509	CGCTGACGCTTTGAGAGCTGAAATACATTCATTCGCGCATTAACCCGGGAAAATGCTGCAT	568
QY	551	TTGCGGTTATGAGTGCAGCAGATATGCTTAATGTGATGATACACTTAAGAACATTTAG	610
Db	569	ACAGCGGCAACGCGCGCGCTTGATCGGCGCGCTGAGTCCCGGCAACCGCGGAGCTTG	628
QY	611	AAAGTTAAGTATTCATTTTAGATATGTCATGTCACATTAAGATGATTTATTAAGCTGT	670
Db	629	ACGAATTCGCGGCCCATCTTAGGCTTGCTTTCAATTCGCGATGATTTTTCGATATTG	688
QY	671	ATGTGTATGAGCAAAATTAGTATTAATAAAGTGGCGAGCATCTTGAAAAATATATATAAGTA	730
Db	689	AAGGGCAGAAAGAAAAAATCGGAAAGCGGTGCGAAGCGACCAAAAGCAACAACAAACGA	748
QY	731	CGTACGTGAATTATTAGGAAAAAGATGCGCGCAGAAAGATTAATTGACTTATCATATGAGACG	750
Db	749	CGTATCCAGCGTGTGCTGCTGCTGCCGCGCGCAAGAAAAAGTTGACGTTCCATATTCGAGG	808
QY	791	CAGG	794
Db	809	CGGC	812

```

RESULT 10
US-08-886-466-1
: Sequence 1, Application US/08886466C
: Patent No. 6040165
: GENERAL INFORMATION:
: APPLICANT: Marita, Keishi
: APPLICANT: Ishida, Chika
: APPLICANT: Takeuchi, Yoshie
: APPLICANT: Ohts, Chikara
: APPLICANT: Ohnuma, Shinichi
: APPLICANT: Nishino, Tokuzo
: TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
: FILE REFERENCE: 77670/484
: CURRENT APPLICATION NUMBER: US/08/886,466C
: CURRENT FILING DATE: 1997-07-10
: EARLIER APPLICATION NUMBER: JP 8-191635
: EARLIER FILING DATE: 1996-07-03
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 1
: LENGTH: 894
: TYPE: DNA
: ORGANISM: Bacillus stearothermophilus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(891)
US-08-886-466-1

Query Match      18.1%; Score 155.6; DB 3; Length 894;
Best Local Similarity 50.9%; Pred. No. 3, 2e-29;
Matches 399; Conservative 0; Mismatches 37; Indels 6; Gaps 1

QY      17 TGAATTAATTAATGATGAAAGTCATATATGAAATTATCGGTTGCGATTAATTAATCAGTAA 76
DB      29 TCAACGCGCAAAAAACGGCGGTGGAACAAGCGCTCTCCGTTATATAGAGGCTTAAG 88
QY      77 TGAATATCAGCAGTAGAAGAAAGATATGTTATTCATTAATAGTCTGAGATTAAGCATCC 136
DB      89 GCGCGCGGAAGCTGAAAAAAGGCGATGCGTACTTCATTGAGGCGCGGCAAAACGATCC 148
QY      137 GACCAATTCCTGTTATACACTCTTACCTTACCTACTAATACGAGATATAGTTAGTATGA 156
DB      149 GTCCGTTCGCTTCCTGTCACCGCTGGCGGCGCTGGCAAAACCCGGCGGTGAGATTGC 208

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Qy	19	AGAGCCAAATTGCACTAGAAATGATTCATACATTTCACTTAATTCAGATGACCTACAG	256
Db	209	CCGTCGCCCTGGCCGANTGAAATGATCCATAGTACTCTTTGATCCATGATGATTTGCCA	268
Qy	257	CGATGGATTAATGATGATTATTCGACGAGGAAATTAACAATCATTAAGTATATGCTGAGT	316
Db	269	GCATGGACAACATATATTTGGCCGCGGCAAGCCGAGAACATTAAGTGTTCGGCGAGG	328
Qy	317	GGACTCGAATTATGAGGTGATGCTTTATTAACCTAAAGCATTTGAATTATTC-----	371
Db	329	CGATGGCCATCTTTGGCGGGGACGGGTGTTGACGTACGCTTTCATTTATGACCGAA	388
Qy	372	-AAGTATATATGATTAATCTGATGTAAGTAAATTAAGTTCTACACAGGCTGCAATAG	430
Db	389	TCGACGATAGCGCATCCCTCCTTCCTCGTCCGGCTTCGGCTCATCGAACGGCTGGCGAAG	448
Qy	431	CAAGTGTGATGTTGAAATGTCGGCGGCTCAATGTTAATATGCAAAAGCGAAGCCAC	490
Db	449	CGCGCCGTCGGAAGGGATGTCGCGCGGCTCAGCGACGCCATATGAAAGGAGGGGAAA	508
Qy	491	CAATTATCTTGAAACTTTGGAAATGATACACAAACAAAACGAGACATTATTTAACTT	550
Db	509	CGCTGACGCTTCGAGAGCTCGAATACATTCATCGGCAATAAACGGGAAATGCTGCAAT	568
Qy	551	TTGCGGTTATGAGTGCACGATATCGCTTAATGTGCATGATCAACTTAAGAACATTAG	610
Db	569	ACAGCGCTGACGCGCGCGCTTGATCGCGGCGGTGATGCCCGGCAAAACGCGGAGCTTG	628
Qy	611	AAAGTATATGTTATCATTTAGTGATGATGTCCAGATTTAAAGATTTTATAGCTGCT	670
Db	629	ACGAATTCGCGCGCCATCTTAGCGCTTGCTTTCAAAATTCGGATGATATCTCGATATTG	688
Qy	671	ATGCTATATGAACCAAGTTAGTATAAAAGTGGGCAACGATCTTGAAATTAATAAAGTA	730
Db	689	AAAGGGCAAAAGAAAAATCGCAAGCCGTCGGGAGGACCAAGCAACAACAAAGCGA	748
Qy	731	CGTACCTGAGTTTATTAAGGAAAGATGCGCGAGAAAGTAAATTGACTTATCATAGACG	790
Db	749	CGTATCCACGTTGCTGTGCTTGCGCGGCGGAAGGAAAGTTGCGCTTCATATCGAGG	808
Qy	791	CAGC 794	
Db	809	CGGC 812	

```

US-09-475-304-1
RESULT 11
Sequence 1, Application US/09475304
Patent No. 6225096
GENERAL INFORMATION:
APPLICANT: Narita, Keishi
APPLICANT: Ishida, Chika
APPLICANT: Takeuchi, Yoshie
APPLICANT: Oho, Chikara
APPLICANT: Ohnuma, Shinichi
APPLICANT: Nishino, Tokuzo
TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
FILE REFERENCE: 77670/494
CURRENT APPLICATION NUMBER: US/09/475,304
CURRENT FILING DATE: 1999-12-30
EARLIER APPLICATION NUMBER: JP 8-191635
EARLIER FILING DATE: 1996-07-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 894
TYPE: DNA
ORGANISM: Bacillus stearothermophilus
FEATURES:
NAME/KEY: CDS
LOCATION: (1)...(891)
US-09-475-304-1

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Query Match 18.1%; Score 155.6; DB 3; Length 894;
Best Local Similarity 50.9%; Pred. No. 3.2e-29;
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

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17 TGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGTGCGATTAATTAATCAAGTA 76
29 TCAACGAGCAAAAACGCGGTGGAACACGCGCTCCCGGTATATAGAGCGCTTAAG 88
77 TGAATTAATCACTAGTGAAGAAAGTATGTTTATTAATTAATCTGAGGTAAAGCATCC 136
89 GGCAGGCGAAGCTGAAAAAGGCGATGCGTACTCAATTGAGCGCGCAAAACCAATCC 148
137 GACCAATGCTGATTAATCACTTAATGATTAATCACTTAATGAGTAAAGTAAAGTAA 196
149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGGCAAAACCGCGCGTGGATTGC 208
197 AGAGCGCAATTCGACTAGAAATGATTCATACATATTCATTAATGATGATGATGATG 256
209 CCGTCCGCTGCGCGATTAATGATTCATACGATCTTGTATCATGATGATGATGATG 268
257 CCAATGATTAATGATTAATTCACACGAGAAATTAACAAATCATTAAGTATGATGAT 316
269 GCAATGACAAAGTATGATTTGCGCGCGGCAAGCGCAAGCAATTAAGTATGATGATG 328
317 GCACTGCAATTAAGAGGATGATGCTTTATTAATTAAGCAATTAATGATTAATTC- 371
329 CCAATGCGCATTTGCGCGGAGAGCGGTTTGAAGTACCGCTTTCAATTAATGATGATG 388
372 -AAGTATGATTAATTAATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 430
389 TCGACGATGAGCGATCCCTCCCTCCGCTTCGCTCATGACGCGTGGGAAAG 448
431 CAAGTATGATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGATG 490
449 CGGCGGCTGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
491 CAATGATCTTGAATCTTTGAAATGATTAACAAACAAACAGAGCATTAATTAATCT 550
509 CGGTGCGCTTCGAGCTGCAATACATTCATCGGATTAACCGGAAATGCTGCAAT 568
551 TTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 610
569 ACAGCGTGAAGCGCGCGCTTGAATGCGCGCGTGAATGCGCGCAACCGCGAGCTTG 628
611 AAGTATGATTAATCACTTAATGATGATGATGATGATGATGATGATGATGATGATG 670
629 ACGAATTCGCGCGCATTCAGGCTTCCTTCAATTCGCGATGATTAATTCGATTTG 688
671 ATGATGATGAAGCAATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 730
689 AAGGCGCAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 748
731 CGTACGATGATTAATTAATGAGAAAGATGCGCAGAAAGATTAATTAATTAATTA 790
749 CGATTCAGCGCTTCTGCTGCTTTCGCGCGCGCAAGAAAGTATGATGATGATG 808
791 CAGC 794
809 CGGC 812
```

RESULT 12
US-09-101-126-4

Sequence 4, Application US/09101126
Patent No. 6316216
GENERAL INFORMATION:
APPLICANT: OHTO, CHIKARA
APPLICANT: NAKANE, HIROYUKI
APPLICANT: NISHINO, TOKUZO
APPLICANT: OHNUMA, SHINICHI
APPLICANT: HIROOKA, KAZUTAKE
TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES

FILE REFERENCE: 77670/566
CURRENT APPLICATION NUMBER: US/09/101,126
CURRENT FILING DATE: 1999-04-27
EARLIER APPLICATION NUMBER: PCT/JP97/03921
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: JP 8-307506
EARLIER FILING DATE: 1996-11-05
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentm Ver. 2.0
SEQ ID NO 4
LENGTH: 894
TYPE: DNA
ORGANISM: Bacillus stearothermophilus
FEATURE:
OTHER INFORMATION: 256-276 is an Asp-rich coding domain
US-09-101-126-4

Query Match 18.1%; Score 155.6; DB 4; Length 894;
Best Local Similarity 50.9%; Pred. No. 3.2e-29;
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

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17 TGAATTAATTAATGATGAAGTCAATTAATGAATTAATCGGTGCGATTAATTAATCAAGTA 76
29 TCAACGAGCAAAAACGCGGTGGAACACGCGCTCCCGGTATATAGAGCGCTTAAG 88
77 TGAATTAATCACTAGTGAAGAAAGTATGTTTATTAATTAATGCTGAGGTAAAGCATCC 136
89 GGCAGGCGAAGCTGAAAAAGGCGATGCGTACTCAATTGAGCGCGCAAAACCAATCC 148
137 GACCAATGCTGATTAATCACTTAATGATTAATCACTTAATGAGTAAAGTAAAGTAA 196
149 GTCCGTTGCTGCTTCTGTCACCGCTTCGCGCGCTCGGCAAAACCGCGCGTGGATTGC 208
197 AGAGCGCAATTCGACTAGAAATGATTCATACATATTCATTAATGATGATGATGATG 256
209 CCGTCCGCTGCGCGATTAATGATTCATACGATCTTGTATCATGATGATGATGATG 268
257 CCAATGATTAATGATTAATTCACACGAGAAATTAACAAATCATTAAGTATGATGAT 316
269 GCAATGACAAAGTATGATTTGCGCGCGGCAAGCGCAAGCAATTAAGTATGATGATG 328
317 GCACTGCAATTAAGAGGATGATGCTTTATTAATTAAGCAATTAATGATTAATTC- 371
329 CCAATGCGCATTTGCGCGGAGAGCGGTTTGAAGTACCGCTTTCAATTAATGATGATG 388
372 -AAGTATGATTAATTAATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 430
389 TCGACGATGAGCGATCCCTCCCTCCGCTTCGCTCATGACGCGTGGGAAAG 448
431 CAAGTATGATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGATG 490
449 CGGCGGCTGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
491 CAATGATCTTGAATCTTTGAAATGATTAACAAACAAACAGAGCATTAATTAATCT 550
509 CGGTGCGCTTCGAGCTGCAATACATTCATCGGATTAACCGGAAATGCTGCAAT 568
551 TTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 610
569 ACAGCGTGAAGCGCGCGCTTGAATGCGCGCGTGAATGCGCGCAACCGCGAGCTTG 628
611 AAGTATGATTAATCACTTAATGATGATGATGATGATGATGATGATGATGATGATG 670
629 ACGAATTCGCGCGCATTCAGGCTTCCTTCAATTCGCGATGATTAATTCGATTTG 688
671 ATGATGATGAAGCAATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 730
689 AAGGCGCAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 748
731 CGTACGATGATTAATTAATGAGAAAGATGCGCAGAAAGATTAATTAATTAATTA 790
749 CGATTCAGCGCTTCTGCTGCTTTCGCGCGCGCAAGAAAGTATGATGATGATG 808
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QY 791 CAGC 794
 Db 809 CGGC 812

RESULT 13

US-09-367-528A-4
 / Sequence 4, Application US/09367528A
 / Patent No. 6395525
 / GENERAL INFORMATION:
 / APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
 / TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
 / FILE REFERENCE: PH-586
 / CURRENT APPLICATION NUMBER: US/09/367,528A
 / PRIOR FILING DATE: 1999-08-16
 / PRIOR APPLICATION NUMBER: JP97/346686
 / NUMBER OF SEQ ID NOS: 6
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 4
 / LENGTH: 894
 / TYPE: DNA
 / ORGANISM: Bacillus stearothermophilus
 / FEATURES:
 / NAME/KEY: CDS
 / LOCATION: (1)..(894)
 / US-09-367-528A-4

Query Match 18.1%; Score 155.6; DB 4; Length 894;
 Best Local Similarity 50.9%; Pred. No. 3.2e-29;
 Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

QY 17 TGAATAATTATAGATGAAGTCAATATGATATGCGTTGGCATTAATTAATCACTAA 76
 Db 29 TCAACGACAAACACAGCCGCTGGAACAGCGCTCCCTGATATAGACCGCTTAGAAG 88
 QY 77 TGAATATCTGCTAGTGAAGAAAGTATGTTATATCATTAATGCTGAGAGTAACGATCC 136
 Db 89 GGGCGGGGAGGCTGAAACAGCGGATGCGTATCTGATGAGCGCGGGAACGAACTCC 148
 QY 137 GACCATGTTCTGTATTAATCACTTAATTAATCACTTAATCACTTAATCACTTAATCA 196
 Db 149 GTCCGTGCTGCTCTCTGTCACCGTTGGGGGCTCGGCAAGACCGCGGCTGGATTCG 208
 QY 197 AGAGCGAATTGCACTAGAAATGATTAATCAATATTAATCACTTAATCACTTAATCA 256
 Db 209 CCGTGGCTGCGCATTAATGATGATCACTGATCTTTGATCAATGATGATTTGCGCA 268
 QY 257 CGATGATTAATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 316
 Db 269 GCAATGACAAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 328
 QY 317 GGAATGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 371
 Db 329 CGATGCGCATCTTGGCGGGGACCGGTTGATGATGATGATGATGATGATGATGATGAT 388
 QY 372 -AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 430
 Db 389 TCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 448
 QY 431 CAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490
 Db 449 CGGCGGCGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
 QY 491 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 550
 Db 509 CGCTGACGCTTTCGAGCTCGAATATGATGATGATGATGATGATGATGATGATGATGAT 558
 QY 551 TTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
 Db 569 AAGAGTGCACGCGCGGCTTGTATCGGCGGCTGATGATGATGATGATGATGATGATGAT 628
 QY 611 AAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 670

Db 629 ACGAATTCGCCGCCATCTAGGCTTGCCTTTCAATTCGCGATGATATCTGATATTG 688
 QY 671 ATGATGATGAAGCAAGTATGATTAATAAAGTGGGACGATCTTGAATAATTAATAAGTA 730
 Db 689 AAGGGGCAAGAAAGAAATCGCAAGCCGCTCGGCAACGACCAAGCAACAAACGCGA 748
 QY 731 CGTACGTGATGTTATTTAGGGAAGATGCGGCAAGAAATTAATGATGATGATGATGATG 790
 Db 749 CGATTCACGCTTCTGCTGCTTCCCGCGGCAAGAAAGTTGCGCTTCCATTCGAGG 808
 QY 791 CAGC 794
 Db 809 CGGC 812

RESULT 14

US-08-534-910B-1
 / Sequence 1, Application US/08534910B
 / Patent No. 5766911
 / GENERAL INFORMATION:
 / APPLICANT: KOIKE, Ayumi
 / APPLICANT: OBATA, Shusei
 / APPLICANT: NISHINO, Tokuzo
 / APPLICANT: OHNUMA, Shinichi
 / APPLICANT: NAKAZAWA, Takeshi
 / APPLICANT: OGURA, Kyozo
 / APPLICANT: KOYAMA, Tanetsuchi
 / TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
 / TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding The
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Kenyon & Kenyon
 / STREET: 1025 Connecticut Avenue, N.W., Suite 600
 / CITY: Washington
 / STATE: DC
 / COUNTRY: U.S.
 / ZIP: 20036-5405
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.25" Floppy Disk
 / COMPUTER: IBM PC Compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
 / SOFTWARE: IBM/Word Perfect 6.1 Windows
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/534,910B
 / FILING DATE: 28-SEP-1995
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: JP 7-25253
 / FILING DATE: 14-FEB-1995
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Tofenetti, Judith L.
 / REGISTRATION NUMBER: 39,048
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202)429-1776
 / TELEFAX: (202)429-0796
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 894 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / MOLECULE TYPE: DNA
 / ORIGINAL SOURCE:
 / ORGANISM: Bacillus stearothermophilus
 / US-08-534-910B-1

Query Match 17.9%; Score 154; DB 1; Length 894;
 Best Local Similarity 50.8%; Pred. No. 7.8e-29;
 Matches 398; Conservative 0; Mismatches 380; Indels 6; Gaps 1;
 QY 17 TGAATAATTATAGATGAAGTCAATATGATATGCGTTGGCATTAATTAATCACTAA 76

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Db      29 TCAACGAGCAAAAACAGCGGTGAAAACAGCGCTCTCCCGTATATATAGCGCTTAGAG 88
Qy      77 TGGATATCTAGCTAGAAAGAAATATGTTGATTCATTAATGCTGAGGTAACGATCC 136
Db      89 GCGCGCGCAAGCTGAAAAAGCGATGGCGTACTCATTTGAGGCGCGGCAACGAAATCC 148
Qy      137 GACCGATCTGTATTAATCACTTAAATCACTAAATACGAGATAGATAGTAGTATGA 196
Db      149 GTCCGTGCTGCTTCTGTCACCGCTTCCGCGCTGAAAACCCGCGCTGCAATTGC 208
Qy      197 AGAGCGCAATTCACATGAAATGATTCATATCACTTCACTTAATGATGACCTACAG 256
Db      209 CCGTCCGCTGCGGATGAAATGATTCATACGACCTCTTGTATCATATGATTTGCCGA 268
Qy      257 CGATGATATATGATTTATCGACGAGGAAATTAACAATCATATAATATATATGTTAGT 316
Db      269 GCAATGACACAGATGATTTGCGCGCGGCAAGCCGACGAAACCAATAAAGTTGCGGAGG 328
Qy      317 GCACTGCGATATTAGCAGGTGATGCTTTATTAATAAGCACTTGAATTTTC----- 371
Db      329 CCAATGCGCATCTTGGCGGGGAGCGGGTGTGACGTACGCTTCAATTCATGATCAACGAA 388
Qy      372 -AAGTATATGATTAATCACTGATGAATGAAATTAATAAGTTTACACGCGCTGTCAATAG 430
Db      389 TCGACATGAGCGCATCCCTCCCTCCGCTCCGCTCATCGACGCGTGGCGAAAG 448
Qy      431 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
Db      449 CCGCGCGCTCGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
Qy      491 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
Db      509 CCGTACGCTTTCGAGCTCGAATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 568
Qy      551 TTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
Db      569 ACAAGCTGACGCGCGCGCTTGTATGCGCGCGCTGATGCGCGCAACCGCGGAGCTTG 628
Qy      611 AAAGTTATATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
Db      629 ACGAATTCGCGCGCATCTAGGCTTGCCTTCAATTCGCGATATTCGATATG 688
Qy      671 ATGCTGATGAAGCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730
Db      689 AAGGGGCAAGAAAAATCGGCAAGCCGCTGCGACGAGCAACAAACAAAGCGA 748
Qy      731 CGTACGTGATTTATTAATGAGGAAAGATGCGCAGAAAGATTAATGATGATGATGATGATGATGATGATGAT 790
Db      749 CGTATCCAGCGTTGCTGCTGCTGCTGCGCGCGAGAAAGTTGCGCTTCCATATCGAGG 808
Qy      791 CAGC 794
Db      809 CGGC 812

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RESULT 15

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US-09-367-528A-2
; Sequence 2, Application US/09367528A
; Patent No. 6395525
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 894
; TYPE: DNA

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ORGANISM: Bacillus stearothermophilus

FEATURE:

NAME/KEY: CDS

LOCATION: (1) .. (894)

US-09-367-528A-2

Query Match 17.9%; Score 154; DB 4; Length 894;

Best Local Similarity 50.8%; Pred. No. 7,8e-29;

Matches 398; Conservative 0; Mismatches 380; Indels 6; Gaps 1;

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Qy      17 TGAATAATTAATGATGAAGTCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 76
Db      29 TCAACGCAAAAACAGCGGTGAAAACAGCGCTCTCCCGTATATATAGCGCTTAGAG 88
Qy      77 TGGATATCTAGCTAGAAAGAAATATGTTGATTCATTAATGCTGAGGTAACGATCC 136
Db      89 GCGCGCGCAAGCTGAAAAAGCGATGGCGTACTCATTTGAGGCGCGGCAACGAAATCC 148
Qy      137 GACCGATCTGTATTAATCACTTAAATCACTAAATACGAGATAGATAGTAGTATGA 196
Db      149 GTCCGTGCTGCTTCTGTCACCGCTTCCGCGCTGAAAACCCGCGCTGCAATTGC 208
Qy      197 AGAGCGCAATTCACATGAAATGATTCATATCACTTCACTTAATGATGACCTACAG 256
Db      209 CCGTCCGCTGCGGATGAAATGATTCATACGACCTCTTGTATCATATGATTTGCCGA 268
Qy      257 CGATGATATATGATTTATCGACGAGGAAATTAACAATCATATAATATATATGTTAGT 316
Db      269 GCAATGACACAGATGATTTGCGCGCGGCAAGCCGACGAAACCAATAAAGTTGCGGAGG 328
Qy      317 GCACTGCGATATTAGCAGGTGATGCTTTATTAATAAGCACTTGAATTTTC----- 371
Db      329 CCAATGCGCATCTTGGCGGGGAGCGGGTGTGACGTACGCTTCAATTCATGATCAACGAA 388
Qy      372 -AAGTATATGATTAATCACTGATGAATGAAATTAATAAGTTTACACGCGCTGTCAATAG 430
Db      389 TCGACATGAGCGCATCCCTCCCTCCGCTCCGCTCATCGACGCGTGGCGAAAG 448
Qy      431 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
Db      449 CCGCGCGCTCGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
Qy      491 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
Db      509 CCGTACGCTTTCGAGCTCGAATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 568
Qy      551 TTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
Db      569 ACAAGCTGACGCGCGCGCTTGTATGCGCGCGCTGATGCGCGCAACCGCGGAGCTTG 628
Qy      611 AAAGTTATATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
Db      629 ACGAATTCGCGCGCATCTAGGCTTGCCTTCAATTCGCGATATTCGATATG 688
Qy      671 ATGCTGATGAAGCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730
Db      689 AAGGGGCAAGAAAAATCGGCAAGCCGCTGCGACGAGCAACAAACAAAGCGA 748
Qy      731 CGTACGTGATTTATTAATGAGGAAAGATGCGCAGAAAGATTAATGATGATGATGATGATGATGATGATGAT 790
Db      749 CGTATCCAGCGTTGCTGCTGCTGCTGCGCGCGAGAAAGTTGCGCTTCCATATCGAGG 808
Qy      791 CAGC 794
Db      809 CGGC 812

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Job time : 115 secs

Tue Apr 20 12:43:38 2004

us-09-925-637-63_1.rnpb

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
9283.408 Million cell updates/sec

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Perfect score: 861
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861	100.0	861	9	US-09-925-637-63
2	861	100.0	861	15	US-10-084-205-63
3	861	100.0	1893	8	US-08-781-986A-155
4	861	100.0	1893	13	US-10-329-624-155
5	854.6	99.3	882	13	US-10-282-122A-8179
6	846.6	98.3	882	9	US-09-815-242-8485
7	831.6	96.6	864	9	US-09-815-242-4184
8	449.8	52.2	879	13	US-10-282-122A-34531
9	444.2	51.6	879	13	US-10-282-122A-35068
10	413	48.0	413	9	US-09-815-242-2822
11	413	48.0	413	13	US-10-282-122A-5390
12	337	39.1	337	9	US-09-815-242-3275
13	337	39.1	337	13	US-10-282-122A-5841
14	252.6	29.3	882	13	US-10-282-122A-24756

15	239.8	27.9	5635	16	US-10-398-221-3823	Sequence 3823, Ap
16	231.2	26.9	495269	16	US-10-398-221-8	Sequence 8, Appl1
17	231.2	26.9	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
18	230	26.7	882	13	US-10-282-122A-16522	Sequence 16522, A
19	227.6	26.7	882	13	US-10-282-122A-17062	Sequence 17062, A
20	220	25.6	891	16	US-10-369-493-40236	Sequence 40236, A
21	218.6	25.4	885	16	US-10-369-493-41045	Sequence 41045, A
22	214.6	24.9	870	13	US-10-282-122A-15342	Sequence 15342, A
23	213.6	24.8	888	13	US-10-282-122A-21306	Sequence 21306, Ap
24	198.4	23.0	879	9	US-10-282-122A-21105	Sequence 21105, A
25	196.8	22.9	882	9	US-09-815-242-6533	Sequence 6533, Ap
26	195	22.6	7528	9	US-09-070-927A-55	Sequence 55, Appl
27	175.2	20.3	873	13	US-10-282-122A-38448	Sequence 38448, A
28	174.8	20.3	858	16	US-10-369-493-42078	Sequence 42078, A
29	174.4	20.3	783	16	US-10-369-493-33397	Sequence 33397, A
30	164	19.0	811	9	US-09-974-300-1015	Sequence 1015, Ap
31	163.2	19.0	927	16	US-10-369-493-42439	Sequence 42439, A
32	161.2	18.7	819	16	US-10-369-493-46888	Sequence 46888, A
33	155.6	18.1	894	13	US-10-462-698A-75	Sequence 75, Appl
34	151.6	17.6	795	13	US-10-282-122A-21259	Sequence 21259, A
35	150.6	17.5	930	16	US-10-369-493-43609	Sequence 43609, A
36	150.2	17.4	888	16	US-10-369-493-24167	Sequence 24167, A
37	142.6	16.6	921	13	US-10-282-122A-32509	Sequence 32509, A
38	142.2	16.5	867	13	US-10-282-122A-36078	Sequence 36078, A
39	141.6	16.4	888	16	US-10-369-493-44860	Sequence 44860, A
40	138	16.0	870	16	US-10-369-493-44580	Sequence 44580, A
41	137	15.9	984	16	US-10-369-493-45179	Sequence 45179, A
42	134.6	15.6	888	13	US-10-282-122A-30834	Sequence 30834, A
43	134.4	15.6	847	16	US-10-264-213-81	Sequence 81, Appl
44	134.4	15.6	5805	16	US-10-264-213-116	Sequence 116, Ap
45	131.4	15.3	888	9	US-09-815-242-7142	Sequence 7142, Ap

ALIGNMENTS

RESULT 1
US-09-925-637-63
Sequence 63, Application US/09925637
Patent No. US2002010338A1
GENERAL INFORMATION:
APPLICANT: ChOI
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: PB560
CURRENT APPLICATION NUMBER: US/09/925, 637
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/151,933
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781,986
PRIOR FILING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-637-63
Query Match 100.0%; Score 861; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACGATCTTACCGATGATTAATTAATGATGAAGTCAATTAATGATGCGTTCG 60
Db 1 ATGACGATCTTACCGATGATTAATTAATGATGAAGTCAATTAATGATGCGTTCG 60
QY 61 AATAAATAACGATTAATGATGATCTGAGTAAGAAAGTATGTTGATTCATTAATGCT 120

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Db      61  ATAAATTAATCAAGTAATGATGACTCAGCTAGAAAGAAAGTAATGATTCATTAATGCT 120
QY      121  GGAGGTAAGCGATCCGACCAAGTCTGTATATACACTTATGATTCATTAATGCT 180
Db      121  GGAGGTAAGCGATCCGACCAAGTCTGTATATACACTTATGATTCATTAATGCT 180
QY      181  TATGAGTTAGGTATGAAGACCGCAATGCACTAGAAATGATTCATTAATGCT 240
Db      181  TATGAGTTAGGTATGAAGACCGCAATGCACTAGAAATGATTCATTAATGCT 240
QY      241  CATGATGACCTACCAAGGATGATTAATGATTAATGCAAGAAATTAATCAATCAT 300
Db      241  CATGATGACCTACCAAGGATGATTAATGATTAATGCAAGAAATTAATCAATCAT 300
QY      301  AAGGTAATGCTAGTGAAGCTGCGATATTAGCAAGTATCTTTAATTAAGCAATT 360
Db      301  AAGGTAATGCTAGTGAAGCTGCGATATTAGCAAGTATCTTTAATTAAGCAATT 360
QY      361  GAATCTATTTCAAGTATGATTAATTAATCAATGAATTAATTAATTAATTAATTA 420
Db      361  GAATCTATTTCAAGTATGATTAATTAATCAATGAATTAATTAATTAATTAATTA 420
QY      421  CTGTCAATAGCAAGTGTGATGTTGGAATGCTCGCGCTCAATGTTAGTATGCAAGC 480
Db      421  CTGTCAATAGCAAGTGTGATGTTGGAATGCTCGCGCTCAATGTTAGTATGCAAGC 480
QY      481  GAAGGCCAACCAATTGATCTTGAACCTTGGAAATGATACCAAAACAAAACAGAGCA 540
Db      481  GAAGGCCAACCAATTGATCTTGAACCTTGGAAATGATACCAAAACAAAACAGAGCA 540
QY      541  TTAATTAATCTTGGGTTATGATGAGCAAGATGATGCTAATGATGATCAACTAA 600
Db      541  TTAATTAATCTTGGGTTATGATGAGCAAGATGATGCTAATGATGATCAACTAA 600
QY      601  GAACTATTAGAAAGTTATAGTTATCAATTAATGATGATGATGATGATGATGATGAT 660
Db      601  GAACTATTAGAAAGTTATAGTTATCAATTAATGATGATGATGATGATGATGATGAT 660
QY      661  TTGACATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db      661  TTGACATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY      721  AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db      721  AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY      781  CATGAGACGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db      781  CATGAGACGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
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Db      841  TTATTAGAAATCGTTGATTTA 861

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RESULT 2
US-10-084-205-63
; Sequence 63, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, G.H.
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P815P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 63

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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-084-205-63

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Query Match      100.0%; Score 861; DB 15; Length 861;
Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  ATAAATTAATCAAGTAATGATGACTCAGCTAGAAAGAAAGTAATGATTCATTAATGCT 120
QY      121  GGAGGTAAGCGATCCGACCAAGTCTGTATATACACTTATGATTCATTAATGCT 180
Db      121  GGAGGTAAGCGATCCGACCAAGTCTGTATATACACTTATGATTCATTAATGCT 180
QY      181  TATGAGTTAGGTATGAAGACCGCAATGCACTAGAAATGATTCATTAATGCT 240
Db      181  TATGAGTTAGGTATGAAGACCGCAATGCACTAGAAATGATTCATTAATGCT 240
QY      241  CATGATGACCTACCAAGGATGATTAATGATTAATGCAAGAAATTAATCAATCAT 300
Db      241  CATGATGACCTACCAAGGATGATTAATGATTAATGCAAGAAATTAATCAATCAT 300
QY      301  AAGGTAATGCTAGTGAAGCTGCGATATTAGCAAGTATCTTTAATTAAGCAATT 360
Db      301  AAGGTAATGCTAGTGAAGCTGCGATATTAGCAAGTATCTTTAATTAAGCAATT 360
QY      361  GAATCTATTTCAAGTATGATTAATTAATCAATGAATTAATTAATTAATTAATTA 420
Db      361  GAATCTATTTCAAGTATGATTAATTAATCAATGAATTAATTAATTAATTAATTA 420
QY      421  CTGTCAATAGCAAGTGTGATGTTGGAATGCTCGCGCTCAATGTTAGTATGCAAGC 480
Db      421  CTGTCAATAGCAAGTGTGATGTTGGAATGCTCGCGCTCAATGTTAGTATGCAAGC 480
QY      481  GAAGGCCAACCAATTGATCTTGAACCTTGGAAATGATACCAAAACAAAACAGAGCA 540
Db      481  GAAGGCCAACCAATTGATCTTGAACCTTGGAAATGATACCAAAACAAAACAGAGCA 540
QY      541  TTAATTAATCTTGGGTTATGATGAGCAAGATGATGCTAATGATGATGATGATGATGAT 600
Db      541  TTAATTAATCTTGGGTTATGATGAGCAAGATGATGCTAATGATGATGATGATGATGAT 600
QY      601  GAACTATTAGAAAGTTATAGTTATCAATTAATGATGATGATGATGATGATGATGATGAT 660
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QY      661  TTGACATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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Db      721  AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY      781  CATGAGACGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db      781  CATGAGACGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY      841  TTATTAGAAATCGTTGATTTA 861
Db      841  TTATTAGAAATCGTTGATTTA 861

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RESULT 3
US-08-781-986A-155/C
; Sequence 155, Application US/08781986A

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Publication No. US20030054436A1
 GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PB248BP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 155:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1893 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-155

Query Match 100.0%; Score 861; DB 8; Length 1893;
 Best Local Similarity 100.0%; Pred. No. 2.3e-177;
 Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGAATCTACCGCATGAATTAATTAATAGATGAGTCATTAATGAAATTCGCTGGC 60
 DB 1314 ATGAGGAATCTACCGCATGAATTAATTAATAGATGAGTCATTAATGAAATTCGCTGGC 1255

QY 61 ATAAATTAATCATGTAATGATGATCTAGCTAGAGAAAGTATGTTGATTCATTAATGCT 120
 DB 1254 ATAAATTAATCATGTAATGATGATCTAGCTAGAGAAAGTATGTTGATTCATTAATGCT 1195

QY 121 GGAGGTAAACGATCCGACCAAGTTCTGTTATTAATCTACTTAAATCACTAAATACCGAG 180
 DB 1194 GGAGGTAAACGATCCGACCAAGTTCTGTTATTAATCTACTTAAATCACTAAATACCGAG 1135

QY 131 TATGATGATGATTAATTAAGCGCAATTCGCTAGAAAGTATTCATCATTAATGCTATT 240
 DB 1134 TATGATGATGATTAATTAAGCGCAATTCGCTAGAAAGTATTCATCATTAATGCTATT 1075

QY 241 CATGATGACCTACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 1074 CATGATGACCTACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015

QY 301 AAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 1014 AAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955

QY 361 GAACTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 954 GAACTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895

QY 421 CTGTCAATGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

DB 894 CTGTCAATGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835

QY 481 GAAGGCCAACCAATGATCTTGAAACTTTGGAAATGATCACAAAACAAAACAGAGACA 540

DB 834 GAAGGCCAACCAATGATCTTGAAACTTTGGAAATGATCACAAAACAAAACAGAGACA 775

QY 541 TATTAATCTTTGGCGGTTATGAGTGCAGAGATATCGTAATGTCGATGATCAATTA 600

DB 774 TATTAATCTTTGGCGGTTATGAGTGCAGAGATATCGTAATGTCGATGATCAATTA 715

QY 601 GAACTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

DB 714 GAACTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655

QY 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

DB 654 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595

QY 721 AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

DB 594 AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535

QY 781 CATAGAGCGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

DB 534 CATAGAGCGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475

QY 841 TTATTGAAATCGTTGATTTA 861

DB 474 TTATTGAAATCGTTGATTTA 454

RESULT 4
 US-10-329-624-155/c
 Sequence 155, Application US/10329624
 Publication No. US20040043037A1
 GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/329,624
 FILING DATE: 27-Dec-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/956,171
 FILING DATE: October 20, 1997
 APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/781,986
 FILING DATE: January 3, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439

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; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1893 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-10-329-624-155

Query Match      100.0%; Score 861; DB 13; Length 1893;
Best Local Similarity 100.0%; Pred. No. 2.3e-177;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGAATCTACCGATGAAATTAATTAATAGATGAAGTCAATATATGATATCGGTTGGC 60
DB 1314 ATGACGAATCTACCGATGAAATTAATTAATAGATGAAGTCAATATATGATATCGGTTGGC 1255

QY 61 ATAAATTAATCAGTAATGATGATCTAGCTAGAGAAAGATGTTGATTCATTAATGCT 120
DB 1254 ATAAATTAATCAGTAATGATGATCTAGCTAGAGAAAGATGTTGATTCATTAATGCT 1195

QY 121 GGAGTAAACGATCCGACAGTTCTGTTATCTACTACTTATAGATTCACTAATACCGAG 180
DB 1194 GGAGTAAACGATCCGACAGTTCTGTTATCTACTACTTATAGATTCACTAATACCGAG 1135

QY 181 TATGATTTAGGTATGAAGACCGCAATTGCACTAGAAATGATTCATATTCATTTACTATT 240
DB 1134 TATGATTTAGGTATGAAGACCGCAATTGCACTAGAAATGATTCATATTCATTTACTATT 1075

QY 241 CATGATGACCTACCGAGATGATGATATGATATGATATGATGATGATGATGATGATGAT 300
DB 1074 CATGATGACCTACCGAGATGATGATATGATATGATATGATGATGATGATGATGATGAT 1015

QY 301 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 1014 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955

QY 361 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 954 GAATCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895

QY 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 894 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835

QY 481 GAAGGCCAACCAATTGATCTTGAACTTTGGAATGATGATGATGATGATGATGATGATGAT 540
DB 834 GAAGGCCAACCAATTGATCTTGAACTTTGGAATGATGATGATGATGATGATGATGATGAT 775

QY 541 TTATTAATCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 774 TTATTAATCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715

QY 601 GAACATTTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 714 GAACATTTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655

QY 661 TTAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 654 TTAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595

QY 721 AATTAAGTACGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 594 AATTAAGTACGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 535

QY 781 CATAGAGACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 534 CATAGAGACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475

QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 474 TTATTAAGAAATCGTTGATTTA 454
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RESULT 5
US-10-282-122A-8179
; Sequence 8179, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EP/17A.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8179
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-8179

Query Match      99.3%; Score 854.6; DB 13; Length 882;
Best Local Similarity 99.5%; Pred. No. 4.2e-176;
Matches 857; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACGAATCTACCGATGAAATTAATTAATAGATGAAGTCAATATATGATATCGGTTGGC 60
DB 1 ATGACGAATCTACCGATGAAATTAATTAATAGATGAAGTCAATATATGATATCGGTTGGC 60

QY 61 ATAAATTAATCAGTAATGATGATCTAGCTAGAGAAAGATGTTGATTCATTAATGCT 120
DB 61 ATAAATTAATCAGTAATGATGATCTAGCTAGAGAAAGATGTTGATTCATTAATGCT 120

QY 121 GGAGTAAACGATCCGACAGTTCTGTTATCTACTACTTATAGATTCACTAATACCGAG 180
DB 121 GGAGTAAACGATCCGACAGTTCTGTTATCTACTACTTATAGATTCACTAATACCGAG 180

QY 181 TATGATTTAGGTATGAAGACCGCAATTGCACTAGAAATGATTCATATTCATTTACTATT 240
DB 181 TATGATTTAGGTATGAAGACCGCAATTGCACTAGAAATGATTCATATTCATTTACTATT 240

QY 241 CATGATGACCTACCGAGATGATGATATGATATGATATGATGATGATGATGATGATGAT 300
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QY 841 TTATTAGAAATCGTTGATTTA 861
DB 841 TTATTAGAAATCGTTGATTTA 861

RESULT 7

US-09-815-242-4184
Sequence 4184, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zysek, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4184
LENGTH: 864
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-815-242-4184

Query Match 96.6%; Score 831.6; DB 9; Length 864;
Best Local Similarity 98.9%; Pred. No. 4.2e-171;
Matches 837; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 ATGATATAATTAAGATGAAGTCAATATGATTAATCGTTGCGATTAATTAATCAGTA 75
DB 1 ATGATATAATTAAGATGAAGTCAATATGATTAATCGTTGCGATTAATTAATCAGTA 60
QY 76 ATGATATACTAGCTAGAAAGATGTTGTTATTCATTAATGCTGAGGTAACCGATC 135
DB 61 ATGATATACTAGCTAGAAAGATGTTGTTATTCATTAATGCTGAGGTAACCGATC 120
QY 136 CGACCAAGTCTGTTATTAATCACTTATGATCACTAATACCGAGTATGAGTATG 195
DB 121 CGACCAAGTCTGTTATTAATCACTTATGATCACTAATACCGAGTATGAGTATG 180
QY 196 AAGAGCGCAATGCACTAGAAATGATTCATATCACTTATTCATGATGACCTACCA 255
DB 181 AAGAGCGCAATGCACTAGAAATGATTCATATCACTTATTCATGATGACCTACCA 240
QY 256 GCGATGATTAATGATTAATGATGAGGAAATTAATCAATCAATAGTAATGAGTATG 315
DB 241 GCGATGATTAATGATTAATGATGAGGAAATTAATCAATCAATAGTAATGAGTATG 300
QY 316 TGAATGCGATTAATGAGGATGATGCTTATTAATCAATAGGATTTGATTTCAAGT 375
DB 301 TGAATGCGATTAATGAGGATGATGCTTATTAATCAATAGGATTTGATTTCAAGT 360

QY 376 GATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 435
DB 361 GATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 436 GGTGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 495
DB 421 GGTGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 496 GATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAAT 555
DB 481 GATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAAT 540
QY 556 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 615
DB 541 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 616 TATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 675
DB 601 TATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 676 GATGAGCAAAAGTTAGTAAAGTGGGCAAGCTCTTGAATTAATTAATTAATTAATTAAT 735
DB 661 GATGAGCAAAAGTTAGTAAAGTGGGCAAGCTCTTGAATTAATTAATTAATTAATTAAT 720
QY 736 GTGAGTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 795
DB 721 GTGAGTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 796 GTGAGTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 855
DB 781 GTGAGTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 856 GATTTA 861
DB 841 GATTTA 846

RESULT 8

US-10-282-122A-34531
Sequence 34531, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zysek, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931

Query Match	52.2%;	Score 449.8;	DB 13;	Length 879;
Best Local Similarity	70.2%;	Pred. No. 5.1e-88;		
Matches 604; Conservative	0;	Mismatches 257;	Indels 0;	Gaps 0;

Qy	1	ATACCAATCTCCCGATGAATTAATTAATGATGAAGCAATATGAAATTCGGTTGG	60
Db	1	ATGAAGAACTCAAGTGAATTAATTAATTAATTAATCACTGAAATGATGA	60
Qy	61	ATTAATTAATTCAGTAAATGATCTCAGCTAGAAGAAATGTTGTAATCATTAATTCG	120
Db	61	ATTCATATCATCCATTTAAAAATTAATTTAGAAAGAAAGTGAATTTTCATTAATTCG	120
Qy	121	GGAGGTAAACGATCCGACCACTTCGTATTACTCATTTAGATTCACTAAATACCGAG	180
Db	121	GGTGTAAAGATCGACCACTCATTAATTAATTAACATTAATAATGCTTAAACAAAGT	180
Qy	181	TATAGTTAGTATGAGAGCGCAATTCACCTAAGAAATGATCATATTCATCTATT	240
Db	181	TATCAACAAGACTAAATAGTCTTTAGCACTGSAATAGATCATACTTAATTCCTTAAT	240
Qy	241	CATGATGACCTTACCCGATGATATGATGATTAATGACGAGAAATTAACAAATCAT	300
Db	241	CAGATGATTTACGACCAATGGATATATACATTAACCGTGAAGAAATTAACAAATCAT	300
Qy	301	AAAGTATATGAGAGTGGACCTGATATTAACAGCTATTCCTTAATTAACCTAAAGATT	360
Db	301	AAAGTTATATGAGAAATGGAAACCATTTCTGTGTATGATATTAACAAAGCTTTT	360
Qy	361	GAACTTATTTCAAGTATGATGATTAACCTGATGAAATTAATAAAGTTCTACACCG	420
Db	361	GAATTAGTTTCTAATGATACTACATGSAATAGTGTGAAGTAAATGATTAATTAAGAA	420
Qy	421	CTGTCAATGCAAGTGTCTATGTTGAAATGTCGCGCGTCAAAATGTTAGATGCAAGC	480
Db	421	CTTTCAAAAGCAAGTGCACATTTGGGAATGTCGTGGTCCCAACGCTGTGATGGAAGT	480
Qy	481	GAAAGCAACAATGATCTTGAAACTTGGAAATGATACAAACCAAAAACGAGAGA	540
Db	481	GAAAGCAATCATTCGTTTGAAACTTTAGAACTTAATGAACTAAAGACGAGCGT	540
Qy	541	TATTAACCTTTGCGGTATAGTGCACAGATATCGCTAATGCTGATGATCAACTAAA	600
Db	541	TATCTAAATTTTTCAGTTATGCGCTGCGGTACACTGCTCAATGAAACAAATATGCT	600
Qy	601	GAAACATTTGAAAGTTATAGTATCATTTAGATATGATGTTCCAGATTAAGATGATTA	660
Db	601	AAAGATTTAGATGAATTTAGTCATCATTTAGGAATGATGTTTCAAAATTAAGATGATTTA	660
Qy	661	TTAGACTGCTATGATGATGAAGCAAAAGTTAGTATTAATAAATGGGACGACATCTGAAAT	720
Db	661	CTGAGATGTATATGATGATGAATCAAACTTGGCAAAAATGAGCGATGATATAGTAAAT	720
Qy	721	AAATAAAGTACGTACGTAGTTTATAGGAAGATGCGCAGAGAATTAATTCGCTTAT	780
Db	721	CATTAAGTACTTATGTTCTTTACTTGAAATTAAGAGACAGAGAAAAGTTAAACAT	780
Qy	781	CATAGAGCGCACGATGATGAACTAACGAAATGATGATCAATTCATACAAACAC	840
Db	781	CATCATATCTTGCTATAGACTGCTTAATCAATTAATTTCTGATCAATATGATCTTCTGA	840

RESULT 9
US-10-282-122A-35068

```

Publication No. US60040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Walli, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELTPA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35066
LENGTH: 879
TYPE: DNA
ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35066

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	Query Match	Similarity	Score	DB	Length
	Best	Local	51.6%	444.2	879
	Matches	559	Conservative	0	Mismatches 258, Indels 0, Gaps 0
QY	1	ATGACGAATCTACCGATGAATTAATTATGATGAAGTCATATGAAATATTCGGTTGGC	60		
Db	1	ATGCGAAGAAGTCATGATGATTAATTAATCAATTATATGCGCTTGCAGGATGA	60		
QY	61	ATAAATAATCAGTAATGATCTCAGCTTGAGAAAGATGTTGTGATTCATTAATGCT	120		
Db	61	ATCGAACTTACACCACTAAATACGAATCTTGAGAAAGATGCAAAATTCCTCATATGG	120		
QY	121	GGAGGTAAACCATTCGACAGCTCTGTATTAATCACTTAGATCACTAATAATACGAG	180		
Db	121	GGTGTAAAGAAATTAAGCCACTTCTGTATTTTAAACATGATGATTAATAATCAAGAT	180		
QY	181	TATGATGATGATGAAGAGCGCATTTGACATGAAATGATTCATCATATTCCTACTATT	240		

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Db      181 TATATAAAGGTAAAAAAGTGCATGGCATTTGGAAATGATTCACAGTATCTTTAAAT 240
Qy      241 CATATATACCTACAGGATGATGATTAATGATTAATGACAGAGAAATTAACAATCAT 300
Db      241 CATATATATCTTCTTGGAATGATTAATGATTAATGATTAATGATTAATGATTAAT 300
Qy      301 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db      301 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy      361 GAACTTTATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db      361 GAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy      421 CTGTCAATGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db      421 TTACGCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy      481 GAAAGCCAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db      481 GAAATATTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy      541 TTATTAATCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGAT 600
Db      541 TTATCTCAATTCGAGATTTAGTGCAGCTGATTTCTTAAAGTATGATGATGAT 600
Qy      601 GAACATTTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db      601 CAAGCTCTGGAAGATTTAGTATGATGATGATGATGATGATGATGATGATGAT 660
Qy      661 TTAACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db      661 CTGACGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy      721 AATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db      721 CACAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy      781 CATGAGACGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db      781 CATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy      841 TTATTAAGAAATCGTTGA 857
Db      841 CTATTAATGATATCGTTGA 857
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```
RESULT 10
US-09-815-242-2822/c
; Sequence 2822, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
```

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Db      181 TATATAAAGGTAAAAAAGTGCATGGCATTTGGAAATGATTCACAGTATCTTTAAAT 240
Qy      241 CATATATACCTACAGGATGATGATTAATGATTAATGACAGAGAAATTAACAATCAT 300
Db      241 CATATATATCTTCTTGGAATGATTAATGATTAATGATTAATGATTAATGATTAAT 300
Qy      301 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db      301 AAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy      361 GAACTTTATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db      361 GAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy      421 CTGTCAATGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db      421 TTACGCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy      481 GAAAGCCAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db      481 GAAATATTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy      541 TTATTAATCTTTGCGGTTATGATGATGATGATGATGATGATGATGATGATGAT 600
Db      541 TTATCTCAATTCGAGATTTAGTGCAGCTGATTTCTTAAAGTATGATGATGAT 600
Qy      601 GAACATTTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db      601 CAAGCTCTGGAAGATTTAGTATGATGATGATGATGATGATGATGATGATGAT 660
Qy      661 TTAACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db      661 CTGACGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy      721 AATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db      721 CACAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy      781 CATGAGACGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db      781 CATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy      841 TTATTAAGAAATCGTTGA 857
Db      841 CTATTAATGATATCGTTGA 857
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RESULT 11
US-10-282-122A-5390/c
; Sequence 5390, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyn, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
```

```

FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3275
LENGTH: 337
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-815-242-3275

Query Match      39.1%; Score 337; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.2e-63;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      225  TACGATTCCTTTCATGATGACCCACGAGCATGGATGATGATGATGATGACGAG 284
DB      337  TACGATTCCTTTCATGATGATGACCCACGAGCATGGATGATGATGATGATGACGAG 278

OY      285  AAAATTAACAATCATAAAGTATGATGATGATGATGATGATGATGATGATGATGATG 344
DB      277  AAAATTAACAATCATAAAGTATGATGATGATGATGATGATGATGATGATGATGATG 218

OY      345  ATTACGTAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 404
DB      217  ATTACGTAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 158

OY      405  AAAAGTTCTCAACGGGTGTCATATGCAAGTGTGATGATGATGATGATGATGATGATG 464
DB      157  AAAAGTTCTCAACGGGTGTCATATGCAAGTGTGATGATGATGATGATGATGATGATG 98

OY      465  GTTAGATATGCAAGCGGACCAACCAATGATGATGATGATGATGATGATGATGATGATG 524
DB      97  GTTAGATATGCAAGCGGACCAACCAATGATGATGATGATGATGATGATGATGATGATG 38

OY      525  AACAAAAACGAGCATTTATTTGCGGTATG 561
DB      37  AACAAAAACGAGCATTTATTTGCGGTATG 1

RESULT 13
US-10-282-122A-5841/c
Sequence 5841, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zysek, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

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QY 541 TTATTAACCTTTGGCGTTATGATGACAGATATCGCTAAATGTCGATGATACACTAAA 600
DB 547 TTATTAATTTTATGCTGTAACCTCTGACGCAAAAATTCGGGAAGCTGATCCGAAACAAAG 606
QY 601 GAACATTTAGAAAGTTATATGTTATCATTTAGGTATGATGTTCCAGATTTAAAGATGATTTA 660
DB 607 AAACCTTACGAAATTTTTCAGAGAAATATTTGGGATTTGCAATTTAGCGACGATATTT 666
QY 661 TTAGACTGCTATGATGATGAGCAAGTTAGGTAATAAAGTGGCGAGGATCTTGAAAT 720
DB 667 TTAGATGATATTTGGATGATAACGAAAATGGGTAAAGACAGAGGGCCGACGCTTTTCTG 726
QY 721 AATAAAGTACGCTACGCTGATGATTTATTTAGGGAAGAATGGCGAGAGATATAATTTGACTTAT 780
DB 727 AATAAAGTACCTATCCCGGATTTACTCAAGCTTGATGGGGGCAAAAAGGCATTTAAATGAG 786
QY 781 CAT 783
DB 787 CAT 789

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RESULT 15

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US-10-398-221-3823
/ Sequence 3823, Application US/10398221
/ Publication No. US20040018514A1
/ GENERAL INFORMATION:
/ APPLICANT: KUNST, Frederik
/ APPLICANT: GLASER, Philippe
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ CURRENT FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: FR 00/12 697
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 3823
/ LENGTH: 5635
/ TYPE: DNA
/ ORGANISM: Listeria monocytogenes 4b
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(end)
/ OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3823

```

Query Match 27.9%; Score 239.8; DB 16; Length 5635;

Best Local Similarity 58.2%; Pred. No. 5.4e-42; Matches 421; Conservative 0; Mismatches 302; Indels 0; Gaps 0;

```

QY 61 AATAAATAATCATGATATGATATCTAGCTAGAGAAAGTATGTTGATTCATTAATGCT 120
DB 2944 AATAACGAGCGAAATATGAACTAGACTAAAGAGTCCATGTTATATCTGTTCAAGCA 3003
QY 121 GGAAGTAAACGATCCGACCACTTCTGTTATTTACTCATCTTAGATTCCTAAATACGAG 180
DB 3004 GGTGAAACGAGATTCGCTCCATGCTAGTTTGTCTACACTTCAAGCCTTAAGATAAT 3063
QY 181 TATGAGTTAGTATGAGAGCGCAATGCACTAGAAATGATTCATATCATATTTCACTTAT 240
DB 3064 CCGCTTTTGTGTGAAAACAGCAACGGGCTTAGAAATGATTCATACGTATAGCCTGATC 3123
QY 241 CATGATGACCTTCCAGCGATGATATATGATTTATGACAGAGAAATTAACAATCAT 300
DB 3124 CATGATGATTTACCGACATGATATATGATCTATCTGCGGCAAAATATATCTATATCAT 3183
QY 301 AAAGTATATGATGATGAGCTGCGATTTAGCAGGTGATGCTTTTATTAATAAGCATTT 360
DB 3184 AAAGTTTTGGGAGTGAACATGCGATTTTGGCAGAGAGAGCGTTTACTAAGCGTTGCTTTT 3243
QY 361 GAACCTTATTTCAAGTATGATGATTAAGTATGATGAAATATAAAGTTCTTACACGG 420

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DB 3244 TCATTTTACCGGAACAGCAAAATTTATCTTTTGAACAGCATACCTTTGATTAATCA 3303
QY 421 CTGTCAATAGCAAGTGTCTATGTTGAATGTTGGGGTCAAAATGTTAGATATGCAAGC 480
DB 3304 ATTAGTTTATGATGTTGTCAGAAAGATGTTGGGGTCAAACTTTCAGATATGAGGCA 3363
QY 481 GAAGCCAAACCAATGATCTTGAACCTTGAATATGATACAAACAAACAGAGCA 540
DB 3364 GAAACAAACAAAGTACATTTAGAAACTATCTCATCTCATGACAGGAAACAGGCGAA 3423
QY 541 TTATTAATTTTGGGTTATGATGTCAGAGATATGCTATGTCATATGATATCACTTAA 600
DB 3424 TTATTAATTTTCCGTAACCTTCTGCTGCAAAATGACAGAGCTGACCCGGAACAAAG 3483
QY 601 GAACATTTAGAAAGTTATAGTTATCATTTTATGATATGTTCCAGATTTAAAGATATTA 660
DB 3484 AAAGATTAAGGATTTTGGGAAATATTTGGGATTTGATTCGAAATTCAGCGAGATTT 3543
QY 661 TTAGCTGCTATGATGATGAGCAAAAGTTAGTAAATAAGTGGCAGCGATCTTGAAAT 720
DB 3544 TTAGATGTTATTTGTTGATGAAACAAATGGGTAAATAAGCAGGGGTGACGCTTTCTG 3603
QY 721 AATAAAGTACGTAAGTATTTATTTAGGGAAGAATGGCGCAGAAATATTTGACTTAT 780
DB 3604 AACAAAAGTACCTATCCCGATTTACTCAAGCTTGATGTTGCCAAAGGGCATTTAAATGAG 3663
QY 781 CAT 783
DB 3664 CAT 3666

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Search completed: April 20, 2004, 08:07:54
Job time : 432 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2004, 15:49:03 ; Search time 23 Seconds
(without alignments)
644.202 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 287

Sequence: 1 MTNIPMNLTIDVNNELSLVA.....ELTQIDQFNTKHLLEIVDL 287

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents_AA:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	35.5	293	3	US-09-276-873-2
2	37	12.9	302	4	US-09-134-001C-3171
3	17	5.9	280	4	US-09-634-238-303
4	17	5.9	312	4	US-09-107-532A-6724
5	15	5.2	297	4	US-09-934-903-14
6	15	5.2	307	4	US-09-543-681A-5908
7	14	4.9	297	1	US-08-534-910B-7
8	14	4.9	297	1	US-08-534-910B-8
9	14	4.9	297	1	US-08-534-910B-10
10	14	4.9	297	3	US-08-886-466-2
11	14	4.9	297	3	US-09-475-304-2
12	14	4.9	297	4	US-09-101-126-3
13	14	4.9	297	4	US-09-367-528A-5
14	11	3.8	291	3	US-09-275-742-2
15	9	3.1	320	3	US-09-217-609A-6
16	9	3.1	320	3	US-08-873-235B-6
17	9	3.1	342	4	US-09-540-225-2512
18	9	3.1	342	4	US-09-540-225-2512
19	8	2.8	219	4	US-09-328-352-5590
20	8	2.8	226	4	US-09-148-545-145
21	8	2.8	285	3	US-09-187-050-12
22	8	2.8	293	2	US-08-284-465-4
23	8	2.8	294	2	US-08-284-465-3
24	8	2.8	294	2	US-08-284-465-8
25	8	2.8	297	1	US-08-534-910B-6
26	8	2.8	297	1	US-08-534-910B-9
27	8	2.8	297	4	US-09-367-528A-1
					Sequence 3, Appli

28	8	2.8	299	4	US-09-489-039A-12733	Sequence 12733, A
29	8	2.8	393	3	US-09-187-050-2	Sequence 2, Appli
30	8	2.8	393	3	US-09-187-050-14	Sequence 14, Appli
31	8	2.8	393	3	US-09-187-050-16	Sequence 16, Appli
32	8	2.8	393	3	US-09-187-050-18	Sequence 18, Appli
33	8	2.8	393	3	US-09-187-050-20	Sequence 20, Appli
34	8	2.8	393	3	US-09-187-050-22	Sequence 22, Appli
35	8	2.8	393	3	US-09-187-050-24	Sequence 24, Appli
36	8	2.8	393	3	US-09-187-050-26	Sequence 26, Appli
37	8	2.8	393	3	US-09-187-050-28	Sequence 28, Appli
38	8	2.8	393	3	US-09-187-050-29	Sequence 29, Appli
39	8	2.8	393	3	US-09-187-050-30	Sequence 30, Appli
40	8	2.8	393	3	US-09-187-050-31	Sequence 31, Appli
41	8	2.8	393	3	US-09-187-050-32	Sequence 32, Appli
42	8	2.8	393	3	US-09-187-050-33	Sequence 33, Appli
43	8	2.8	393	3	US-09-187-050-34	Sequence 34, Appli
44	8	2.8	393	3	US-09-187-050-34	Sequence 34, Appli
45	8	2.8	401	4	US-09-252-991A-26387	Sequence 26387, A

ALIGNMENTS

RESULT 1
US-09-276-873-2
; Sequence 2, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Widing, Edwina Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: 15A
; FILE REFERENCE: GM10208
; CURRENT APPLICATION NUMBER: US/09/276, 873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-276-873-2

Query Match 35.5%; Score 102; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KLTNKKYGEWTAIILAGDALLTKAFELISSDRLTDEVKIKYQLRSLASGHVGVGGQM 155
DB 96 KLTNKKYGEWTAIILAGDALLTKAFELISSDRLTDEVKIKYQLRSLASGHVGVGGQM 155
QY 156 LDMQSEGPIDLTETEMIKTKTGALLTPYVGAADIANVD 197
DB 156 LDMQSEGPIDLTETEMIKTKTGALLTPYVGAADIANVD 197
RESULT 2
US-09-134-001C-3171
; Sequence 3171, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; CURRENT FILING DATE: 1998-08-13/064, 964
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055, 779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3171
; LENGTH: 302

TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3171

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-28;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMIHTYSLIHDDLPMNDYRKGCTLNKRYGEM 106
79 ALEMIHTYSLIHDDLPMNDYRKGCTLNKRYGEM 115

RESULT 3
US-09-634-238-303
Sequence 303, Application US/09634238
Patent No. 6544772
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Hawukkala, Ilkka J.
APPLICANT: Bloksberg, Leonard, N.
APPLICANT: Lubbers, Mark W.
APPLICANT: Dekker, James
APPLICANT: Christenson, Anna C.
APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
FILE REFERENCE: 11000.104301
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 303
LENGTH: 280
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
US-09-634-238-303

Query Match
Best Local Similarity 5.9%; Score 17; DB 4; Length 280;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMNDND 91
Db 70 HTYSLIHDDLPMNDND 86

RESULT 4
US-09-107-532A-6724
Sequence 6724, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6724:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
MOLECULE TYPE: Protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...312
SEQUENCE DESCRIPTION: SEQ ID NO: 6724:
US-09-107-532A-6724

Query Match
Best Local Similarity 5.9%; Score 17; DB 4; Length 312;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMNDND 91
Db 93 HTYSLIHDDLPMNDND 109

RESULT 5
US-09-934-903-14
Sequence 14, Application US/09934903
Patent No. 6660507
GENERAL INFORMATION:
APPLICANT: Koffas, Matthews
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. 6660507on, Kelley C.
APPLICANT: Tomb, Jean-Francois
APPLICANT: Rouviere, Pierre
APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: C11646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 297
TYPE: PRT
ORGANISM: Methylobionas 16a
OTHER INFORMATION: Amino acid sequences encoded by ORF7
US-09-934-903-14

Query Match
Best Local Similarity 5.2%; Score 15; DB 4; Length 297;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 YSLIHDDLPMNDND 91
Db 80 YSLIHDDLPMNDND 94

RESULT 6
US-09-543-681A-5908
Sequence 5908, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5908
LENGTH: 307
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5908

Query Match 5.2%; Score 15; DB 4; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPAMDND 91
Db 87 YSLIHDDLPAMDND 101

RESULT 7
US-08-534-910B-7
Sequence 7, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534.910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
US-08-534-910B-7

Query Match 4.9%; Score 14; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 EMHTYSLIHDDLP 85
Db 76 EMHTYSLIHDDLP 89

RESULT 8
US-08-534-910B-8
Sequence 8, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding The
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534.910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-8

Query Match 4.9%; Score 14; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 EMHTYSLIHDDLP 85
Db 76 EMHTYSLIHDDLP 89

RESULT 9

US-08-534-910B-10
; Sequence 10, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetsoshi
; TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable
; OF SYNTHESIZING GERANYLERANYLDIPHOSPHATE AND GENE CODING THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
; US-08-534-910B-10

Query Match 4.9%; Score 14; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 EMHTYSLIHDDLP 85
Db 76 EMHTYSLIHDDLP 89

RESULT 10
US-08-886-466-2
; Sequence 2, Application US/08886466C
; Patent No. 6040165
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie

; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/08/886,466C
; CURRENT FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; US-08-886-466-2

Query Match 4.9%; Score 14; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 EMHTYSLIHDDLP 85
Db 76 EMHTYSLIHDDLP 89

RESULT 11
US-09-475-304-2
; Sequence 2, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; CURRENT FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; US-09-475-304-2

Query Match 4.9%; Score 14; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 EMHTYSLIHDDLP 85
Db 76 EMHTYSLIHDDLP 89

RESULT 12
US-08-101-126-3
; Sequence 3, Application US/09101126
; Patent No. 6316216
; GENERAL INFORMATION:
; APPLICANT: OHTO, CHIKARA
; APPLICANT: NAKANE, HIROYUKI
; APPLICANT: NISHINO, TOKUZO
; APPLICANT: OHNUMA, SHINICHI
; APPLICANT: HIROOKA, KAZUTAKE
; TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
; FILE REFERENCE: 77670/566
; CURRENT APPLICATION NUMBER: US/09/101,126

CURRENT FILING DATE: 1999-04-27
; EARLIER APPLICATION NUMBER: PCT/JP97/03921
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: JP 8-307506
; EARLIER FILING DATE: 1996-11-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; OTHER INFORMATION: 86-92 is an Asp-rich domain
US-09-101-126-3

Query Match 4.9%; Score 14; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
|||
Db 76 EMHTYSLIHDDLP 89

RESULT 13
US-09-367-528A-5
; Sequence 5, Application US/09367528A
; Patent No. 6395525
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 5
; TYPE: PRT
; LENGTH: 297
; ORGANISM: Bacillus stearothermophilus
US-09-367-528A-5

Query Match 4.9%; Score 14; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
|||
Db 76 EMHTYSLIHDDLP 89

RESULT 14
US-09-275-742-2
; Sequence 2, Application US/09275742
; Patent No. 6130069
; GENERAL INFORMATION:
; APPLICANT: WILDING, Edwina Imogen
; APPLICANT: GWYN, Michael
; TITLE OF INVENTION: 18PA
; FILE REFERENCE: GMI0205
; CURRENT APPLICATION NUMBER: US/09/275,742
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-275-742-2

Query Match 3.8%; Score 11; DB 3; Length 291;

Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SLIHDDLPAMD 88
|||
Db 76 SLIHDDLPAMD 86

RESULT 15
US-09-217-609A-6
; Sequence 6, Application US/09217609A
; Patent No. 6071733
; GENERAL INFORMATION:
; APPLICANT: MURAMATSU, Masayoshi
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OGURA, Kyozo
; APPLICANT: KOYAMA, Tanecoshi
; APPLICANT: SHIMIZU, Naoto
; APPLICANT: CHO, Yewjin
; TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, NW - Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,609A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/873,235
; FILING DATE: 11-Jun-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: TOFFENETTI, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 10235/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-217-609A-6

Query Match 3.1%; Score 9; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 AGGKRIRPV 48
|||
Db 42 AGGKRIRPV 50

Search completed: April 19, 2004, 15:54:52
Job time : 23 secs

Tue Apr 20 12:43:39 2004

us-09-925-637-64.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2004, 15:53:23 ; Search time 47 Seconds
(without alignments)
1683.366 Million cell updates/sec

Title: US-09-925-637-64

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Gapop 60.0 , Gapext 60.0

Searched: 1124875 seqs, 275673149 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1124875

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Post-processing: Listing first 45 summaries

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Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubppa/US00_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	287	100.0	287	9 US-09-925-637-64	Sequence 64, Appl
2	287	100.0	287	14 US-10-084-205-64	Sequence 64, Appl
3	197	68.6	293	9 US-09-815-242-12583	Sequence 12583, A
4	192	66.9	288	9 US-09-815-242-5239	Sequence 5239, Ap
5	132	46.0	293	12 US-10-282-122A-44363	Sequence 44363, A
6	12.9	293	12	US-10-282-122A-70715	Sequence 70715, A
7	37	12.9	293	12 US-10-282-122A-71252	Sequence 71252, A
8	28	9.8	310	15 US-10-369-493-19922	Sequence 19922, A
9	27	9.4	293	12 US-10-282-122A-60940	Sequence 60940, A
10	22	7.7	261	15 US-10-369-493-9710	Sequence 9710, Ap
11	20	7.0	294	12 US-10-282-122A-52706	Sequence 52706, A
12	18	6.3	285	15 US-10-369-493-18391	Sequence 18391, A
13	18	6.3	290	12 US-10-282-122A-74642	Sequence 74642, A
14	18	6.3	293	9 US-09-815-242-10630	Sequence 10630, A
15	18	6.3	293	12 US-10-282-122A-57289	Sequence 57289, A

16	18	6.3	309	15 US-10-369-493-18752	Sequence 18752, A
17	17	5.9	265	12 US-10-282-122A-57443	Sequence 57443, A
18	17	5.9	280	15 US-10-264-213-206	Sequence 206, App
19	17	5.9	283	15 US-10-264-213-240	Sequence 240, App
20	17	5.9	306	15 US-10-369-493-10187	Sequence 10187, A
21	16	5.6	281	12 US-10-282-122A-54639	Sequence 54639, A
22	15	5.2	287	15 US-10-369-493-19191	Sequence 19191, A
23	15	5.2	289	12 US-10-282-122A-72262	Sequence 72262, A
24	15	5.2	294	12 US-10-282-122A-61262	Sequence 61262, A
25	15	5.2	295	12 US-10-282-122A-53246	Sequence 53246, A
26	15	5.2	296	15 US-10-369-493-480	Sequence 480, App
27	15	5.2	296	15 US-10-369-493-21173	Sequence 21173, A
28	15	5.2	297	9 US-09-934-903-14	Sequence 14, Appl
29	15	5.2	297	9 US-09-934-903-14	Sequence 14, Appl
30	15	5.2	297	9 US-09-934-903-14	Sequence 14, Appl
31	15	5.2	297	12 US-10-700-003-14	Sequence 20, Appl
32	15	5.2	307	12 US-10-282-122A-68693	Sequence 68693, A
33	14	4.9	292	15 US-10-369-493-23201	Sequence 23201, A
34	14	4.9	289	12 US-10-282-122A-51526	Sequence 51526, A
35	14	4.9	294	15 US-10-369-493-17358	Sequence 17358, A
36	14	4.9	297	14 US-10-462-688A-76	Sequence 76, Appl
37	12	4.2	153	15 US-10-369-493-16138	Sequence 16138, A
38	12	4.2	156	15 US-10-369-493-15292	Sequence 15292, A
39	12	4.2	156	15 US-10-369-493-15657	Sequence 15657, A
40	12	4.2	156	15 US-10-369-493-15657	Sequence 15657, A
41	12	4.2	294	12 US-10-282-122A-77172	Sequence 77172, A
42	12	4.2	294	15 US-10-369-493-18010	Sequence 18010, A
43	12	4.2	295	9 US-09-815-242-11239	Sequence 11239, A
44	12	4.2	295	12 US-10-282-122A-58515	Sequence 58515, A
45	12	4.2	295	12 US-10-282-122A-67018	Sequence 67018, A
			298	12 US-10-282-122A-73438	Sequence 73438, A

ALIGNMENTS

US-09-925-637-64
Sequence 64, Application US/09925637
Patent No. US2002010338A1
GENERAL INFORMATION:
APPLICANT: CHOI
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: PB560
CURRENT APPLICATION NUMBER: US 60/151,933
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/151,933
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781,986
PRIOR FILING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 287
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-637-64

Query Match 100.0%; Score 287; DB %; Length 287;
Best Local Similarity 100.0%; Pred. No. 5.2e-269;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPKMKLIDVNNELSYVAIKSVYDQLEBSMLYSNAGGKRIRPVLLITLDSLNT 60
DB 1 MTNLPKMKLIDVNNELSYVAIKSVYDQLEBSMLYSNAGGKRIRPVLLITLDSLNT 60
QY 61 YEAGKSAVALAMITYSILHDDLPAMNDPDRRGKLTNNHKYGGWTAIINGDALTLTAF 120

Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIIAGDALITKAF 120
QY 121 ELISSDDRLEDEVKIKYQLRSLASGHVGVGQMLDMOSEGQPIDLETEMHKTGTGA 180
Db 121 ELISSDDRLEDEVKIKYQLRSLASGHVGVGQMLDMOSEGQPIDLETEMHKTGTGA 180
QY 181 LITFAVMSADIANVDDTTKEHLESYSYHLGMMFQIKDDLLDCYGEAKLGGKVGSDLEN 240
Db 181 LITFAVMSADIANVDDTTKEHLESYSYHLGMMFQIKDDLLDCYGEAKLGGKVGSDLEN 240
QY 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287
Db 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287

RESULT 2
US-10-084-205-64
Sequence 64, Application US/10084205
Publication No. US20030049648A1
GENERAL INFORMATION:
APPLICANT: Choi, Gil
TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P51521
CURRENT APPLICATION NUMBER: US/10/084,205
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/151,933
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO: 64
LENGTH: 287
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-084-205-64

Query Match 100.0%; Score 287; DB 14; Length 287;
Best Local Similarity 100.0%; Pred. No. 5.2e-269;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTNLPNKLIDEVNNELSVAINKSVMDTQLEESMLYSINAGGKIRPVLILLTDSINTE 60
Db 1 MTNLPNKLIDEVNNELSVAINKSVMDTQLEESMLYSINAGGKIRPVLILLTDSINTE 60
QY 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIIAGDALITKAF 120
Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIIAGDALITKAF 120
QY 121 ELISSDDRLEDEVKIKYQLRSLASGHVGVGQMLDMOSEGQPIDLETEMHKTGTGA 180
Db 121 ELISSDDRLEDEVKIKYQLRSLASGHVGVGQMLDMOSEGQPIDLETEMHKTGTGA 180
QY 181 LITFAVMSADIANVDDTTKEHLESYSYHLGMMFQIKDDLLDCYGEAKLGGKVGSDLEN 240
Db 181 LITFAVMSADIANVDDTTKEHLESYSYHLGMMFQIKDDLLDCYGEAKLGGKVGSDLEN 240
QY 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287
Db 241 NKSTYVSLGKDGAEKLTYHRDAVDELTOIDEGFNTKLLLEIVDL 287

RESULT 3
US-09-815-242-12583
Sequence 12583, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 12583
LENGTH: 293
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12583

Query Match 68.6%; Score 197; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 5.8e-182;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTNLPNKLIDEVNNELSVAINKSVMDTQLEESMLYSINAGGKIRPVLILLTDSINTE 60
Db 1 MTNLPNKLIDEVNNELSVAINKSVMDTQLEESMLYSINAGGKIRPVLILLTDSINTE 60
QY 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIIAGDALITKAF 120
Db 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNKKVGEWTAIIAGDALITKAF 120
QY 121 ELISSDDRLEDEVKIKYQLRSLASGHVGVGQMLDMOSEGQPIDLETEMHKTGTGA 180
Db 121 ELISSDDRLEDEVKIKYQLRSLASGHVGVGQMLDMOSEGQPIDLETEMHKTGTGA 180
QY 181 LITFAVMSADIANVDD 197
Db 181 LITFAVMSADIANVDD 197

RESULT 4
US-09-815-242-5239
Sequence 5239, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 5239
LENGTH: 288
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5239

Query Match 66.9%; Score 192; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.9e-177;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NKKLDEVNNEISVAINKSVMDTOLEESMTYSINAGKRIKRPVLLLTLDLSINTEYELGM 65
DB 1 NKKLDEVNNEISVAINKSVMDTOLEESMTYSINAGKRIKRPVLLLTLDLSINTEYELGM 60
QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 125
DB 61 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 120
QY 126 DDLRTDEVKIKVQLRLSLASGHVGVGQMLDMQSEGPIDLETLEMHKTKTGALLTFA 185
DB 121 DDLRTDEVKIKVQLRLSLASGHVGVGQMLDMQSEGPIDLETLEMHKTKTGALLTFA 180
QY 186 VMSADIANVDD 197
DB 181 VMSADIANVDD 192

RESULT 5
US-10-282-122A-44363
Sequence 44363, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 44363
LENGTH: 293
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-44363

Query Match 46.0%; Score 132; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 4.3e-119;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 125
DB 66 KSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNKKYGEWTAILAGDALLTKAFELISS 125
QY 126 DDLRTDEVKIKVQLRLSLASGHVGVGQMLDMQSEGPIDLETLEMHKTKTGALLTFA 185
DB 126 DDLRTDEVKIKVQLRLSLASGHVGVGQMLDMQSEGPIDLETLEMHKTKTGALLTFA 185
QY 186 VMSADIANVDD 197
DB 186 VMSADIANVDD 197

RESULT 6
US-10-282-122A-70715
Sequence 70715, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 70715
LENGTH: 293
TYPE: PRT

ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70715

Query Match 12.9%; Score 37; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMHTYSLIHDDLPMANDNDYRGLTNHKYGE 106
Db 70 ALEMHTYSLIHDDLPMANDNDYRGLTNHKYGE 106

RESULT 7
US-10-282-122A-71252
Sequence 71252, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71252
LENGTH: 293
TYPE: PRT
ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71252

Query Match 12.9%; Score 37; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMHTYSLIHDDLPMANDNDYRGLTNHKYGE 106

Db 70 ALEMHTYSLIHDDLPMANDNDYRGLTNHKYGE 106

RESULT 8
US-10-369-493-19922
Sequence 19922, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 19922

LENGTH: 310

TYPE: PRT

ORGANISM: No. US20030233675A1loc punctiforme

US-10-369-493-19922

Query Match 9.8%; Score 28; DB 15; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.7e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SLIHDDLPMANDNDYRGLTNHKYGE 105
Db 94 SLIHDDLPMANDNDYRGLTNHKYGE 121

RESULT 9
US-10-282-122A-60940
Sequence 60940, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 60940
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-10-282-122A-60940

Query Match
Best Local Similarity 9.4%; Score 27; DB 12; Length 293;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMHTYSLIHDDLPMNDNDYRRGK 96
DB 72 ALEMHTYSLIHDDLPMNDNDYRRGX 98

RESULT 10
; US-10-369-493-9710
; Sequence 9710, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 9710
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Desulfitobacterium hafnense
; US-10-369-493-9710

Query Match
Best Local Similarity 7.7%; Score 22; DB 15; Length 261;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IHTYSLIHDDLPMNDNDYRRG 95
DB 43 IHTYSLIHDDLPMNDNDYRRG 64

RESULT 11
; US-10-282-122A-52706
; Sequence 52706, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangyu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Malone, Cheryl
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
```

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; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 52706
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Clostridium botulinum
; US-10-282-122A-52706

Query Match
Best Local Similarity 7.0%; Score 20; DB 12; Length 294;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLPMNDND 91
DB 75 EMHTYSLIHDDLPMNDND 94

RESULT 12
; US-10-369-493-18391
; Sequence 18391, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 18391
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Lactococcus lactis
; US-10-369-493-18391

Query Match
Best Local Similarity 6.3%; Score 18; DB 15; Length 285;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SLIHDDLPMNDNDYRRG 95
DB 74 SLIHDDLPMNDNDYRRG 91
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RESULT 13
US-10-282-122A-74642
; Sequence 74642, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 74642
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74642

Query Match      6.3%; Score 18; DB 12; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      78 SLIHDDLPAMDNDYRNG 95
Db      75 SLIHDDLPAMDNDYRNG 92

RESULT 14
US-09-815-242-10630
; Sequence 10630, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

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; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10630
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10630

Query Match      6.3%; Score 18; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      71 LEMHTYSLIHDDLPAMD 88
Db      71 LEMHTYSLIHDDLPAMD 88

RESULT 15
US-10-282-122A-57289
; Sequence 57289, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931

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Tue Apr 20 12:43:39 2004

us-09-925-637-64.rapb

Page 7

; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 57289
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-57289

Query Match 6.3%; Score 18; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 LEMHTYSLIHDDLPAMD 88
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Db 71 LEMHTYSLIHDDLPAMD 88

Search completed: April 19, 2004, 15:59:38
Job time : 47 secs

Tue Apr 20 12:43:40 2004

us-09-925-637-64.rnt

Page 1

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 20, 2004, 08:08:02 ; Search time 64 Seconds
(without alignments)
2488.608 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 1453
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 segs, 27475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

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2: /cg2_6/ptodata/2/ina/5B.COMB.seq:*
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4: /cg2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cg2_6/ptodata/2/ina/PTCUS.COMB.seq:*
6: /cg2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1453	100.0	1893	4	US-08-956-171E-155
2	1456	98.8	882	3	US-09-276-873-1
3	1015	69.9	909	4	US-09-134-001C-334
4	657	45.2	894	1	US-08-534-910B-4
5	656	45.1	894	1	US-08-534-910B-5
6	654	45.0	893	1	US-08-534-910B-1
7	653	44.9	894	1	US-08-534-910B-2
8	650	44.7	894	1	US-08-534-910B-3
9	650	44.7	894	1	US-08-886-466-1
10	650	44.7	894	3	US-09-475-304-1
11	650	44.7	894	4	US-09-101-126-4
12	650	44.7	894	4	US-09-367-528A-4

13	645	44.4	894	1	US-08-534-910B-1	Sequence 1, Appl1
14	644	44.3	894	4	US-09-367-528A-2	Sequence 2, Appl1
15	551	37.8	876	3	US-09-275-742-1	Sequence 1, Appl1
C 16	549	37.8	1001.1	4	US-08-961-527-76	Sequence 76, Appl1
17	533	36.7	939	4	US-09-107-532A-3070	Sequence 3070, Ap
18	520.5	35.8	885	3	US-09-187-050-11	Sequence 11, Appl
19	520.5	35.8	1179	3	US-09-187-050-13	Sequence 13, Appl
20	520.5	35.8	1179	3	US-09-187-050-15	Sequence 15, Appl
21	520.5	35.8	1179	3	US-09-187-050-17	Sequence 17, Appl
22	520.5	35.8	1179	3	US-09-187-050-19	Sequence 19, Appl
23	520.5	35.8	1179	3	US-09-187-050-21	Sequence 21, Appl
24	520.5	35.8	1179	3	US-09-187-050-23	Sequence 23, Appl
25	520.5	35.8	1179	3	US-09-187-050-25	Sequence 25, Appl
26	520.5	35.8	1889	3	US-09-187-050-13	Sequence 1, Appl1
27	516.5	35.5	891	4	US-09-334-903-13	Sequence 13, Appl
28	457.5	34.2	1830121	4	US-09-557-884-1	Sequence 1, Appl1
29	457.5	34.2	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
C 30	487.5	33.6	96109	4	US-09-596-002-35	Sequence 35, Appl1
31	482	33.2	924	4	US-09-543-681A-1736	Sequence 1736, Ap
32	481	33.1	1029	4	US-09-540-236-692	Sequence 692, Ap
33	480.5	33.1	900	4	US-09-489-039A-5562	Sequence 5562, Ap
34	480	33.0	847	4	US-09-634-238-85	Sequence 85, Appl
35	474.5	32.7	1071	4	US-09-552-991A-10000	Sequence 10000, A
36	474.5	32.7	1206	4	US-09-552-991A-9816	Sequence 9816, Ap
C 37	474.5	32.7	4515	4	US-09-552-991A-10037	Sequence 10037, A
38	465.5	32.0	1131	4	US-09-420-211-1	Sequence 1, Appl1
39	442	30.4	927	4	US-09-328-352-64	Sequence 64, Appl
40	438.5	30.2	486	3	US-09-217-609A-28	Sequence 28, Appl
41	438.5	30.2	486	3	US-08-573-235B-28	Sequence 28, Appl
42	438	30.1	1087	4	US-09-549-848B-15	Sequence 15, Appl
43	438	30.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
44	405	27.9	1914	4	US-09-634-238-41	Sequence 41, Appl1
45	376.5	25.9	909	1	US-07-783-705A-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-956-171E-155/c
Sequence 155, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Dikette, 3.50 inch, 1.4MB storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956.171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-09-925-637-64 (1-287) x US-08-956-171E-155 (1-1893)
Alignment Scores:
Pred. No.: 2,03e-176 Length: 1893
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4
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QY 21 IleAsnLysSerValMetAspThrGluLeuGluLysSerMetLeuTySerLeuAsnAla 40
DB 1254 ATAATAATATAGTAATAGATCTACCTAGAAAGATATGTTGTTATTCATTAATGCT 1195
QY 41 GlyGlyLysArgGlyLeaGProValLeuLeuLeuLeuThrsLeuAsnThrGlu 60
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QY 61 TyGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTySerLeu 80
DB 1134 TATAGTTAGTTAGTAAGAGGCGCAATGCACTAGAAATGATTCATCACTTATTCCTTAT 1075
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyArgArgGlyLysLeuThrsAsnHis 100
DB 1074 CATATGACCTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
QY 101 LysValTyGlyGlyGluThrAlaIleLeuAlaGlyAspAlaLeuLeuThrsAlaPhe 120
DB 1014 AAAGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
QY 121 GluLeuIleSerSerAspAspArgLeuThrsAspGluValLysIleLysValLeuGlnArg 140
DB 954 GAACCTATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGluMetLeuAspMetGlnSer 160
DB 894 CTGCAATAGCAAGGTCATGTCGATGTCGCGCGCAATGATGATGATGATGATGATGATGAT 835
QY 161 GluGlyGlnProIleAspLeuGluThrsLeuGluMetIleHisLysThrLysThrGlyAla 180
DB 834 GAAGGCCAACCAATGATCTTGAACCTTGGAAATGATCACAAAACAAACAAACAGACGA 775
QY 181 LeuLeuThrsPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrLys 200
DB 774 TTATTAATCTTTGGGGTTATGATGACGACAGATTCCTATATGTCGATGATGATGATGAT 715
QY 201 GluHisLeuGlnSerTySerTyHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
DB 714 GAACCTTTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
QY 221 LeuAspCysTyGlyAspGluAlaLysLeuGlyLysLysValGlySerAspLeuGlnAsn 240
DB 654 TTAAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
QY 241 AsnLysSerThrTyValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTy 260

|||||
DB 594 AATAAAGTACTAGTACTGATTTATAGGAAAGTGGCGGAGAAAGTAATATGACTTAT 535
QY 261 HisArgAspAlaAlaValAspGluLeuThrsGlnIleAspGluGlnPheAsnThrLysHis 280
DB 534 CATAGAGCGCGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
QY 281 LeuLeuGluIleValAspLeu 287
DB 474 TTATTAAGAAATGCTGATTTA 454
RESULT 2
US-09-925-637-64 (1-287) x US-08-956-171E-155 (1-1893)
; Sequence 1, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Wynding, Edwin Imogen
; APPLICANT: Wynding, Michael
; TITLE OF INVENTION: ISPA
; FILE REFERENCE: GMI0208
; CURRENT APPLICATION NUMBER: US/09/276,873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-925-637-64 (1-287) x US-08-956-171E-155 (1-1893)
Alignment Scores:
Pred. No.: 9,43e-175 Length: 882
Score: 1436.00 Matches: 284
Percent Similarity: 99.30% Conservative: 1
Best Local Similarity: 98.95% Mismatches: 2
Query Match: 98.83% Indels: 0
Gaps: 0
US-09-925-637-64 (1-287) x US-08-956-171E-155 (1-1893)
QY 1 MethThrsenLeuPromeAsnLysLeuLleAspGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGACGATCTACCGATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 21 IleAsnLysSerValMetAspThrGluLeuGluLysSerMetLeuTySerLeuAsnAla 40
DB 61 AATAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 41 GlyGlyLysArgGlyLeaGProValLeuLeuLeuLeuThrsLeuAspSerLeuAsnThrGlu 60
DB 121 GAGGTAACCGATCCACAGCTGCTGTATTAATCACTTAGATTCCTAATAATACCGAG 180
QY 61 TyGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTySerLeu 80
DB 181 TATGATTAAGGTAAAGGCGCAATGCACTAGAAATGATTCATCACTTATTCCTTAT 240
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyArgArgGlyLysLeuThrsAsnHis 100
DB 241 CATGATGACCTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 101 LysValTyGlyGlyGluThrAlaIleLeuAlaGlyAspAlaLeuLeuThrsAlaPhe 120
DB 301 AAAGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 121 GluLeuIleSerSerAspAspArgLeuThrsAspGluValLysIleLysValLeuGlnArg 140
DB 361 GAACCTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGluMetLeuAspMetGlnSer 160
DB 421 CTGCAATAGCAAGGTCATGTCGATGTCGCGCGCAATGATGATGATGATGATGATGATGAT 480
QY 161 GluGlyGlnProIleAspLeuGluThrsLeuGluMetIleHisLysThrLysThrGlyAla 180

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Db      481 GAAGGCAACCAATTCATTTGAACTTTGAAATGATACAAACAAACAGAGACA 540
Qy      181 LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLys 200
Db      541 TTATTAACTTTGCGGTATGAGTGACAGCATATCGCTAATGATGATGATCACTAA 600
Qy      201 GIUHSLeuGluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
Db      601 GAACATTTGAAAGATTATGATATCATTTAGGTATGATGATTCACATTTAAAGATTTA 660
Qy      221 LeuAspCysTyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGln 240
Db      661 TTAGACTGCTATGCTATGATAGCAAGTAAGTAAAGAGTGGCAGCGATCTTGAAAT 720
Qy      241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyr 260
Db      721 AATTAAGAGTACGTACGTGATGATTATTAAGGAAAGATGGCGAGAAATTAATGACTTAT 780
Qy      261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
Db      781 CATTAAGAGCAGCAGCTGATGATCACTAAGCAAAATTGATGAACATTCATCAACAAACAC 840
Qy      281 LeuLeuGluIleValAspLeu 287
Db      841 TTATTAGAAATCGTTGATTTA 861

RESULT 3
US-09-134-001C-334
Sequence 334, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lytn Docette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 334
LENGTH: 909
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-334

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Alignment Scores:
Pred. No.: 1,088-120 Length: 909
Score: 1015.00 Matches: 197
Percent Similarity: 82.93% Conservative: 41
Best Local Similarity: 68.64% Mismatches: 49
Query Match: 69.86% Indels: 0
Gaps: 0

```

US-09-925-637-64 (1-287) x US-09-134-001C-334 (1-909)

```

Qy      1 MetThrAsnLeuPheMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
Db      28 ATGAAGAACTACACATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 87
Qy      21 IleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTyrSerLeuAsnAla 40
Db      88 ATACATCATCATCCATTAATAAATTAATTAAGAAAGTAAGAAATTAATTAATTAATTAAT 147
Qy      41 GlyGlyLysArgGlyLeuArgProValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
Db      148 GGTGTAAAGAAATAGACCACTATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 207
Qy      61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80

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Db      208 TATCAACAGACTAAATTAAGTCTTACATTCGAAATGATTCATCACTTAATTTTAAAT 267
Qy      81 HisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgLysLeuThrAsnHis 100
Db      268 CATGATGATTTACAGCAATGATTAATGATGATTAATGATTAATGATTAATGATTAATGATTA 327
Qy      101 LysValTyrGlyGluTyrPheAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
Db      328 AAGTTTATGCTGAATGAAGAAAGCATTCTTGCTGGATGATGATTAATTAACAAAGCTTT 387
Qy      121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
Db      388 GAATTAATGTTCTAATGATTAATCACTTAATGAAGATGATGAAGATGATTAATTAATTAAGA 447
Qy      141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
Db      448 CTTTCAAAGCAAGTGAACATTTGGGAAATGCTGGGCCACCGCTGATATGAAAGT 507
Qy      161 GIUGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
Db      508 GAAGGAGATGCATTCGTTTGAATCTTGAATCAATTCATCAATCAATCAATCAATCAATCAAT 567
Qy      181 LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLys 200
Db      568 TTACTTAATTTTCAGTTATGCTGCTGGCTAGACATTCCTCAATGACAAACAAATATTGCT 627
Qy      201 GIUHSLeuGluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
Db      628 AAGAAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 687
Qy      221 LeuAspCysTyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGln 240
Db      688 CTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
Qy      241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyr 260
Db      748 CATTAAGAGTACTATGATTTCTTACTTGAAGAAAGAGGAGCAGAAAGTAAGTAACAT 807
Qy      261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
Db      808 CATCAATATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 867
Qy      281 LeuLeuGluIleValAspLeu 287
Db      868 TTATGATGATGATGATGATTTA 888

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RESULT 4
US-08-534-910B-4
Sequence 4, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyozo
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylidiphosphate And Gene Coding The
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows

```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofteneft, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-4

Alignment Scores:
Pred. No.: 9 56-75 Length: 894
Score: 657.00 Matches: 133
Percent Similarity: 68.10% Conservative: 57
Best Local Similarity: 47.67% Mismatches: 83
Query Match: 45.22% Indels: 6
Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-4 (1-894)
QY 1 Methrshnleuprometleuileuileaspdlvalasnanleuileuervalaia 20
DB 1 ATGCGCGAGCTTTCATGATGAGACAGTTTCACGACGAAACAGCGCGGGAACAGCG 60
QY 21 IleasnyserValmet-----AspThrGlnleuGlnleuGlnleuSerMetLeuYr 36
DB 61 CTCGCCCGTATATAGAGCGCTTAGAGGCGCGCGAGCTGAAAAAGCGAGCGGCTAC 120
QY 37 Serleuasnlaaglylylylearggileargprovalleuileuileuileuileuapser 56
DB 121 TCATTGAGGCGCGCGGCAACGATCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGCGG 180
QY 57 leuasnhrgrlurlyrgluleuGlyMetLysSerAlaIleAlaIleuGlnMetIleHstr 76
DB 181 CTCGGCAAAAGACCGCGGCGTCGATTCGCCGTCGCCGTCGCGATGAATGATCCATAG 240
QY 77 TySerleuileuileuileuileuileuileuileuileuileuileuileuileuileu 96
DB 241 CACTCTTTCATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 97 leuasnhrshlysvaIyrglyglutpThrAlaIleuGlnleuGlnleuGlnleuGlnleu 116
DB 301 CCGACGAAACCATTAAGAGTTCGCGGAGCGCATGCGCATCTTGGCGGGGAGCGGCTGTTG 360
QY 117 Thrlysalaphegileuileuileuileuileuileuileuileuileuileuileuileu 134
DB 361 ACGTACGCGTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 135 IlelysvaIleuGlnleuSerIleAlaSerGlyHstrValleuMetValleuGlnleu 154
DB 421 CTTCGCGTCATCGACGCGCTGCGAAAGCGCGCGTCGAGAGGAGTGTGCGCGGTGAG 480
QY 155 MetleuaspmetGlnserGlnleuGlnleuGlnleuGlnleuGlnleuGlnleuGlnleu 174
DB 481 GCACCGCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 175 lythrlystrgrlyalaleuileuThrPheAlaValMetSerAlaIleAlaIleAlaIle 194

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DB 541 CGCATAAACCGGAAATCTGCATACAGCGCTGACGCCGCGCCTTGATCGCGCG 600
QY 195 ValaaspThrThrlyGlnleuGlnleuSerTyrseryrhIleuGlyMetMetPhe 214
DB 601 GGTATGCCCGGCAACCGCGAGGCTTGACCAATCGCGCCCATCTGAGCGCTTGT 660
QY 215 Glnlleuysaaspapleuileuileuileuileuileuileuileuileuileuileuileu 234
DB 661 CAAATTCGCGATGATATCTGATATGAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 235 GlyseraaspLeuGlnleuasnlyserThrTyValserleuileuGlylysaaplyala 254
DB 721 GCGACGACGACCAAGACCAACCAAGCGACGATCCAGCGCTGCTGCTGCGCGCGCG 780
QY 255 GlnaaplyleuThrTyHstrArgaapAlaIleValaaspGlnleuThrGlnleuasp 273
DB 781 AAGAAAAGTTGACGTTTCATATCGAGCGCGGCGCGCATTTACGAGCGCGAC 837

RESULT 5
US-08-534-910B-5
Sequence 5, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OZURA, Kyoza
APPLICANT: KOYAMA, Tanetsoshi
TITLE OF INVENTION: Mutated Farmesylidiphosphate Synthase Capable
TITLE OF INVENTION: OF Synthesizing Geranylgeranyldiphosphate And Gene Coding The
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Kenyon & Kenyon
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofteneft, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-5

Alignment Scores:
Pred. No.: 1 286-74 Length: 894
Score: 656.00 Matches: 133

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Db      361  ACGTACCGCTTTCATTGATCAACGAAATGACAGATGAGCGCATCCCTCTCCGCG 420
Qy      135  ILeYValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
          ::::::::::::::::::::
Db      421  CTGGGCTCATGCAACGGCTGGCGAAGCGCGGTCGGAAGAGATGGTCCGCGGTGAG 480
Qy      155  MetLeuAspMetGlnSerGlnGlnGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
          ::::::::::::::::::::
Db      481  GCAGCCGATATGAGAGAGAGGAGAAACGCTGACGTTCCGAGCTCGAATCATTCAT 540
Qy      175  LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsn 194
          ::::::::::::::::::::
Db      541  CGGATATAAACCGGGAAATGCTTCGATACAGCGTGCACCGCGGCTTGATCGCGCG 600
Qy      195  ValAspAspThrThrLysGlnIleLeuGlnSerTyrSerTyrHisLeuGlnMetMetPhe 214
          ::::::::::::::::::::
Db      601  GCTGATGCCCGGCAACGCGGAGCTTGACGAATTCGCCGCCCATCTGAGCCTTGCTT 660
Qy      215  GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysVal 234
          ::::::::::::::::::::
Db      661  CAATTTCGCGATGATATTCGTGATATGAGGGCGCAAGAAAAATCGCGCAAGCGGTC 720
Qy      235  GlySerAspLeuGlnAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
          ::::::::::::::::::::
Db      721  GGCAGCGACCAACCAACCAACCAACGATTCACAGCGTGTGCTGCTGCGCTTGCGCG 780
Qy      255  GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273
          ::::::::::::::::::::
Db      781  AAGAAAAAGTTGGGCTTCATATCGAGCGCGCGCGCATTTACGGAACGCCGAC 837

RESULT 7
US-08-534-910B-2
Sequence 2, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBARA, Shuhei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: Koyama, Taneoshi
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Ther
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenecti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

```

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;
; LENGTH: 894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus

US-08-534-910B-2

Alignment Scores:
Pred. No.: 3.1e-74
Score: 653.00
Percent Similarity: 67.38%
Best Local Similarity: 47.31%
Query Match: 44.94%
DB: 1 Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-2 (1-894)
Qy      1  MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
          ::::::::::::::::::::
Db      1  ATGGCGCAGCTTTCATGTTGAACAGTTTCTCAACGACAAAAACAGCGCGTGGAAACAG 60
Qy      21  IleAsnLysSerValMet-----AspThrGlnLeuGlnGlnSerMetLeuTyr 36
          ::::::::::::::::::::
Db      61  CTCTCCGCTTATATGAGCGCTTAGAAGCGCGCGGAGGAGTGAAGAAAGCATGGCTTAC 120
Qy      37  SerLeuAsnAlaGlyGlyLysArgIleArgProValLeuLeuLeuThrLeuAspSer 56
          ::::::::::::::::::::
Db      121  TCATTGAGAGCGCGCGGCAACGAATCCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy      57  LeuAsnThrGluTyrGlnLeuGlyMetLysSerAlaIleAlaLeuGlnMetIleHisThr 76
          ::::::::::::::::::::
Db      181  CTGGCAAAAGCCCGCGCGATGGCTGCGCGCTGCGCGATGGAATGAAATCATCATCG 240
Qy      77  TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
          ::::::::::::::::::::
Db      241  TACCTCTTGATCCATGATGATTTGCCAGCATGACACAGATGATTCGCGCGCGCAAG 300
Qy      97  LeuThrAsnHisLysValTyrGlyLysThrAlaIleLeuAlaGlyAspAlaLeuLeu 116
          ::::::::::::::::::::
Db      301  CCGACGAACCATTAAGTGTTCGCGAGCGCATGCGCATCTGGCGGGGAGCGGCTTGTG 360
Qy      117  ThrLysAlaPheGluLeuIleSer-----SerAspAspArgLeuThrAspGluValLys 134
          ::::::::::::::::::::
Db      361  ACGTACCGCTTTCATTGATCAACGAAATGACAGATGAGCGCATCCCTCTCCGCG 420
Qy      135  ILeYValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
          ::::::::::::::::::::
Db      421  CTGGGCTCATGCAACGGCTGGCGAAGCGCGGTCGGAAGAGATGGTCCGCGGTGAG 480
Qy      155  MetLeuAspMetGlnSerGlnGlnGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
          ::::::::::::::::::::
Db      481  GCAGCCGATATGAGAGAGAGGAGAAACGCTGACGTTCCGAGCTCGAATCATTCAT 540
Qy      175  LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsn 194
          ::::::::::::::::::::
Db      541  CGGATATAAACCGGGAAATGCTTCGATACAGCGTGCACCGCGGCTTGATCGCGCG 600
Qy      195  ValAspAspThrThrLysGlnIleLeuGlnSerTyrSerTyrHisLeuGlnMetMetPhe 214
          ::::::::::::::::::::
Db      601  GCTGATGCCCGGCAACGCGGAGCTTGACGAATTCGCCGCCCATCTGAGCCTTGCTT 660
Qy      215  GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysVal 234
          ::::::::::::::::::::
Db      661  CAATTTCGCGATGATATTCGTGATATGAGGGCGCAAGAAAAATCGCGCAAGCGGTC 720
Qy      235  GlySerAspLeuGlnAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
          ::::::::::::::::::::
Db      721  GGCAGCGACCAACCAACCAACCAACGATTCACAGCGTGTGCTGCTGCGCTTGCGCG 780
Qy      255  GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273
          ::::::::::::::::::::

```

Db 781 AAGAAAAGTTGGCTTCATATGAGCGCGAGCCGCAATTACGAACGCCGAC 837

RESULT 8

US-08-534-910B-3

Sequence 3, Application US/08534910B

Patent No. 5766911

GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi

APPLICANT: OBATA, Shusei

APPLICANT: NISHINO, Tokuzo

APPLICANT: OHNUMA, Shinichi

APPLICANT: NAKAZAWA, Takeshi

APPLICANT: OGURA, Kyoze

APPLICANT: KOYAMA, Taneoshi

TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable

TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: U.S.

ZIP: 20036-5405

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.25" Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 6.2

SOFTWARE: IBM/Word Perfect 6.1 Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/534,910B

FILING DATE: 28-SEPT-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-25253

FILING DATE: 14-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Toffenetti, Judith L.

REGISTRATION NUMBER: 39,048

REFERENCE/DOCKET NUMBER: 77670/398

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)429-1776

TELEFAX: (202)429-0796

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 894 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

ORGANISM: *Bacillus stearothermophilus*

US-08-534-910B-3

Alignment Scores:

Pred. No.: 7.52e-74 Length: 894

Score: 650.00 Matches: 132

Percent Similarity: 67.03% Conservative: 55

Best Local Similarity: 47.31% Mismatches: 86

Query Match: 44.74% Indels: 6

DB: 1 Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-3 (1-894)

QY 1 MetThrasnleubProwetAenlyLeuileAspGluValAsnAngluleuSerValAla 20

Db 1 ATGGCGAGCTTCAGTTGACAGTTCACAGACCAAAAACAGCGGTGAGAAACAGCG 60

QY 21 ILeasnlySerValMet-----AspThGlnleuGlnleuSerMetLeuTyr 36

Db 61 CTCTCCGATTATATAGACGCGCTTAGAAGGCGCGGACGCTGAGAAAGCGAGTGGCTTC 120

QY 37 SerLeuAsnAlaGlyGlyArgGleArgProValleuLeuLeuThrLeuAspSer 56

Db 121 TCATTGAGGCGCGGCAACGAAATCGCTCCGTTGCTGTCTGTCCACCGCTTCGCG 180

QY 57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaLeuAlaLeuGluMetLeuThr 76

Db 181 CTCGAAAAGACCCGCGGCGTGGATTCGCCGTCCGCTCGCGGATTTGAATGATCATTCG 240

QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96

Db 241 TACTCTTGTGATTCATGATGATTTGCCGAGCATGACACATGATTTGCCGCGCGGACG 300

QY 97 LeuThrAsnHisLysValIlyrGlyGluTyrThrAlaLeuAlaLeuGluMetLeuLeu 116

Db 301 CCGACGAACCATTAAGTTCGCGGAGCGCATTCCTTGCGCGGAGCGGTTGTTG 360

QY 117 ThrLysAlaPheGluLeuLysSer-----SerAspAspArgLeuThrAspGluValLys 134

Db 361 ACGTACGCGTTTCATTTGATTCACCGAAATCGACGATGACGATCCCTTCCTCGCGG 420

QY 135 ILeysValleuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154

Db 421 CTTCGCGTCATCGAACGCGTGGCGAAGCGCGCTCCGAGAGGATGGCCCGCGTACG 480

QY 155 MetLeuAspMetGlnSerGluGlyGlnProIleAspLeuGluThrLeuGluMetLeuHis 174

Db 481 GCAGCCGATATGAGAGAGAGAGGAGGAGAAACGTCGATTCGAGAGCTCGAATATCATTCAT 540

QY 175 LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsn 194

Db 541 CGGTATTAACCGCGGAAATGCTGCATACAGCGCTGACCGCGCGCTTCGATCGCGCGC 600

QY 195 ValAspAspThrThrLysGluHisLeuGluSerTyrSerTyrHisLeuGlyMetPhe 214

Db 601 GCTGATCCCGCGCAACGCGGAGCTTGACGAATTCGCCCGCATTAAGCCTTCGCTTT 660

QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysVal 234

Db 661 CAATTCGCGCATGATTTCTCGATATTCGAGGCGCAAGAAAACCGGCAACCGCGTC 720

QY 235 GlySerAspLeuGluAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254

Db 721 GCGACGCAACCAACCAACCAACGACGATACCGCTTCGCTGCTGCTGCGCGGCGCA 780

QY 255 GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273

Db 781 AAGAAAAGTTGGCTTCATATGAGCGCGAGCCGCAATTACGAACGCCGAC 837

RESULT 9

US-08-886-466-1

Sequence 1, Application US/08886466C

Patent No. 6040165

GENERAL INFORMATION:

APPLICANT: Narita, Keishi

APPLICANT: Ishida, Chika

APPLICANT: Takeuchi, Yoshie

APPLICANT: Ohto, Chikara

APPLICANT: Ohnuma, Shinichi

APPLICANT: NISHINO, Tokuzo

TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE

FILE REFERENCE: 77670/494

CURRENT APPLICATION NUMBER: US/08/886,466C

EARLIER FILING DATE: 1997-07-10

EARLIER APPLICATION NUMBER: JP 8-191635

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 894

TYPE: DNA

ORGANISM: *Bacillus stearothermophilus*

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(891)

US-08-886-466-1

Alignment Scores:

Pred. No.:	7.52e-74	Length:	894
Score:	650.00	Matches:	134
Percent Similarity:	67.78%	Conservative:	49
Best Local Similarity:	49.63%	Mismatches:	85
Query Match:	44.74%	Indels:	2
		Gaps:	1

US-09-925-637-64 (1-287) x US-08-886-466-1 (1-894)

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QY 6 MetAspLeuIleAspGluValAsnGluSerValAlaIleAsnLysSerVal 25
DB 28 CTCACAGCAAAACAGCGCGTGGAAACAGCGCTCTCCGTTATATAGACGCTTAGAA 87
QY 26 MetAspThrGluIleGluIleSerMetLeuTyrsSerLeuAsnAlaGlyIleValArgIle 45
DB 88 GGGCGCGGCAAGCTGAAAGGCGATGCGTACTCATGAGAGCGCGCGCAACGAAATC 147
QY 46 ArgProValIleLeuLeuLeuThrLeuAspSerLeuAsnThrGluIleGluIleMet 65
DB 148 CGTCGGTTGCTGCTTCTGTCACCGCTTCCGCGCAAGACCCGCGCGGATG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrsSerLeuIleHisAspAspLeuPro 85
DB 208 CCCGTCGCTCGCGGATGAAATGATCATACGACTTGTGATCCATGATGATGCGG 267
QY 86 AlaMetAspAsnAspAspTyrsArgGlyIleLeuThrAsnHisLysValTyrglyGlu 105
DB 268 AGCATGCAACAGATGATTTGCGGCGGCGCAAGCGAACCACTAAAGTTCGCGGAG 327
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrIleAlaPheGluIleSer--- 124
DB 328 GCGATGCGCATCTTGGCGGCGGAGCGGTTGACGATGACGATTCATGATTCACGAA 397
QY 125 ---SerAspAspArgLeuThrAspGluValIleLysValLeuGluIleGluSerIle 143
DB 388 ATCAGCAGTGAAGCGCATCCCTCTCCGCTTCCGCTCATCGAACGCGTGGCGAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyIleGluIleMetLeuAspMetGluIleGluIle 163
DB 448 GCGCGCGGTCGCGAAGGATGTCGCGCGTACGACGCGATATGAAAGAGAGGGGAAA 507
QY 164 ProIleAspLeuGluIleThrLeuGluMetIleHisLysThrIleThrGlyAlaLeuLeuThr 183
DB 508 AGCGTACGCTTTCGAGCTCGAATACCTTCATCGCATTAACCGGGAATAAGCTGCA 567
QY 184 PheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrIleGluHisLeu 203
DB 568 TACAGCGTGAAGCGCGGCTTATGCGCGCGCTGATGCCCGCAACCGCGGAGACT 627
QY 204 GluSerTyrsSerTyrsHisLeuGlyMetMetPheGluIleLysAspAspLeuAspCys 223
DB 628 GACGATTCGCGCGCCATCGACCTTCCCTTCAAAATTCGCGATGATTCGATATT 687
QY 224 TyrGlyAspGluAlaLysLeuGlyLysIleValGlySerAspLeuGluAsnLysSer 243
DB 688 GAAAGGCGCAAGAAAGAAATCGCGCAAGCGGTCGCGACGACCAAGCAACAAAGCG 747
QY 244 ThrTyrsAlaSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrsHisAsp 263
DB 748 ACGTATCCAGCGTCTGCTGCTGCTGCGCGCGCAAGAAAGTTCGATTCATATCGAG 807
QY 264 AlaAlaValAspGluLeuThrGluIleAsp 273
DB 808 GCGGCGCAGCGCATTTACGGAACGCCAC 837

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RESULT 10

US-09-475-304-1
 ; Sequence 1, Application US/09475304
 ; Patent No. 6225096
 ; GENERAL INFORMATION:

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/ APPLICANT: Narita, Keisshi
/ APPLICANT: Ishida, Chika
/ APPLICANT: Takeuchi, Yoshie
/ APPLICANT: Ohts, Chikara
/ APPLICANT: Ohnuma, Shinichi
/ APPLICANT: Nishino, Tokuzo
/ TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
/ FILE REFERENCE: 77670/494
/ CURRENT APPLICATION NUMBER: US/09/475,304
/ EARLIER FILING DATE: 1999-12-30
/ EARLIER APPLICATION NUMBER: JP 8-191635
/ EARLIER FILING DATE: 1996-07-03
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(891)
/ US-09-475-304-1

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Alignment Scores:

Pred. No.:	7.52e-74	Length:	894
Score:	650.00	Matches:	134
Percent Similarity:	67.78%	Conservative:	49
Best Local Similarity:	49.63%	Mismatches:	85
Query Match:	44.74%	Indels:	2
		Gaps:	1

US-09-925-637-64 (1-287) x US-09-475-304-1 (1-894)

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QY 6 MetAspLeuIleAspGluValAsnGluSerValAlaIleAsnLysSerVal 25
DB 28 CTCACAGCAAAACAGCGCGTGGAAACAGCGCTCTCCGTTATATAGACGCTTAGAA 87
QY 26 MetAspThrGluIleGluIleSerMetLeuTyrsSerLeuAsnAlaGlyIleValArgIle 45
DB 88 GGGCGCGGCAAGCTGAAAGGCGATGCGTACTCATGAGAGCGCGCGCAACGAAATC 147
QY 46 ArgProValIleLeuLeuLeuThrLeuAspSerLeuAsnThrGluIleGluIleMet 65
DB 148 CGTCGGTTGCTGCTTCTGTCACCGCTTCCGCGCAAGACCCGCGCGGATG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrsSerLeuIleHisAspAspLeuPro 85
DB 208 CCCGTCGCTCGCGGATGAAATGATCATACGACTTGTGATCCATGATGATGCGG 267
QY 86 AlaMetAspAsnAspAspTyrsArgGlyIleLeuThrAsnHisLysValTyrglyGlu 105
DB 268 AGCATGCAACAGATGATTTGCGGCGGCGCAAGCGACCAACATTAAGTTCGCGGAG 327
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrIleAlaPheGluIleSer--- 124
DB 328 GCGATGCGCATCTTGGCGGCGGAGCGGTTGACGATGACGCTTCAATGATTCACGAA 387
QY 125 ---SerAspAspArgLeuThrAspGluValIleLysValLeuGluIleGluSerIle 143
DB 388 ATCAGCAGTGAAGCGATCCCTCTCCGCTTCCGCTCATCGAACGCGTGGCGAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyIleGluIleMetLeuAspMetGluIleGluIle 163
DB 448 GCGCGCGGTCGCGAAGGATGTCGCGCGTACGACGCGATATGAAAGAGAGGGGAAA 507
QY 164 ProIleAspLeuGluIleThrLeuGluMetIleHisLysThrIleThrGlyAlaLeuLeuThr 183
DB 508 AGCGTACGCTTTCGAGCTCGAATACCTTCATCGCATTAACCGGGAATAAGCTGCA 567
QY 184 PheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrIleGluHisLeu 203
DB 568 TACAGCGTGAAGCGCGGCTTATGCGCGCGCTGATGCCCGCAACCGCGGAGACT 627

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QY 204 GlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLeuAspAspLeuLeuAspCys 223
DB 628 GACGAATTCGCCGCCATCTAGCCCTTGCCTTCAAAATCCGAGATGATTTCTGCATATT 687
QY 224 TyrGlyAspGluAlaIleuLeuGlyLysValGlySerAspLeuGluAsnLysSer 243
DB 688 GAAGGGGCGAAGAAAATCGCAGACCGGTCCGCGAGGACCAAGCAACAAACGCG 747
QY 244 ThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263
DB 748 ACGTATCCACGCGTTCGTTCGCTTCGCGCGCGCAAGAAAAGTTGCGCTTCATATCAG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
DB 808 GCGGCGCAGCGCCATTACGGAACGCCGAC 837

RESULT 11
US-09-101-126-4
/ Sequence 4, Application US/09101126
/ Patent No. 6316216
/ GENERAL INFORMATION:
/ APPLICANT: OHTO, CHIKARA
/ APPLICANT: NAKANE, HIROYUKI
/ APPLICANT: NISHINO, TOKUZO
/ APPLICANT: OHMURA, SHINICHI
/ APPLICANT: HIROOKA, KAZUTAKE
/ TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
/ FILE REFERENCE: 77670/566
/ CURRENT APPLICATION NUMBER: US/09/101,126
/ EARLIER FILING DATE: 1999-04-27
/ EARLIER APPLICATION NUMBER: PCT/JP97/03921
/ EARLIER FILING DATE: 1997-10-29
/ EARLIER APPLICATION NUMBER: JP 8-307506
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ OTHER INFORMATION: 256-276 is an Asp-rich coding domain
US-09-101-126-4

Alignment Scores:
Pred. No.: 7, 52e-74 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: 4 Gaps: 1

US-09-925-637-64 (1-287) x US-09-101-126-4 (1-894)
QY 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25
DB 28 CTCACAGACAAACAAACAGCGCGGTGAAACAGCGCTCTCCGTTATATAGAGCGTTAGAA 87
QY 26 MetAspThrGlnLeuGlnGluSerMetLeuTyrSerLeuAsnAlaGlyLysArgIle 45
DB 88 GGGCGCGCGCAAGTGAAGAGCGAGTGGCTCTCATTTGAGAGCGCGCGCAACGAAATC 147
QY 46 ArgProValIleuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluLeuGlyMet 65
DB 148 CCGTCGTCCTCTCTCTGTCACCGTTCGCGCGCTCGGAAAGACCGCGCGTTCGATG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuPro 85
DB 208 CCCGTCGCTGCGCATTTGAATGATCCATACGTACTCTTGATCATGATGATTTGCGG 267
QY 86 AlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGlu 105
DB 268 AACATGAGCAACGATGATTTGCGCGCGCAAGCGCAAGAACATTAAGATTTGCGCGAG 327
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QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSer--- 124
DB 328 GCGATGCGCATCTTGGCGGGGAGCGGTTCTTACGACCGCTTCAATGATGATCACCGAA 387
QY 125 ---SerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIle 143
DB 388 ATCGACGATAGCGCATCCCTCTCCGCTTCGCGCTTCGCTCATCGAACCGCTGCGCAAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSerGlnGlyGln 163
DB 448 GCGCGCGCTCGGAAGGATGTCGCCGTCAGCAGCCGATATGGAAGAGAGGGAAA 507
QY 164 ProLeuAspLeuGluThrLeuGluMetIleHisThrTyrHisThrGlyAlaLeuLeuThr 183
DB 508 ACGCTAGCGCTTCGAGCTCGAATCATTCATTCGGAATAAACCGGAAAATGCTGCAA 567
QY 184 PheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203
DB 568 TACAGCGTCGACCGCGCGCTTGATCGCGCGCTGATGCCGCAACCGCGGAGCTT 627
QY 204 GlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuLeuAspCys 223
DB 628 GACGAATTCGCCGCCATCTAGCCCTTGCCTTCAAAATTCGCAATGATATTCGATATT 687
QY 224 TyrGlyAspGluAlaIleuLeuGlyLysValGlySerAspLeuGluAsnLysSer 243
DB 688 GAAGGGGCGAAGAAAATCGCAGACCGGTCCGCGAGCGACCAACCAACAAACGCG 747
QY 244 ThrTyrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263
DB 748 ACGTATCCACGCTTCGTTCGCTTCGCGCGCGCAAGAAAAGTTGCGCTTCATATCAG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
DB 808 GCGGCGCAGCGCCATTACGGAACGCCGAC 837

RESULT 12
US-09-367-528A-4
/ Sequence 4, Application US/09367528A
/ Patent No. 6395525
/ GENERAL INFORMATION:
/ APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
/ TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
/ FILE REFERENCE: PH-586
/ CURRENT APPLICATION NUMBER: US/09/367,528A
/ EARLIER FILING DATE: 1999-08-16
/ PRIOR APPLICATION NUMBER: JP97/346686
/ EARLIER FILING DATE: 1997-12-16
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(894)
US-09-367-528A-4

Alignment Scores:
Pred. No.: 7, 52e-74 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: 4 Gaps: 1

US-09-925-637-64 (1-287) x US-09-367-528A-4 (1-894)
QY 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25
DB 28 CTCACAGACAAACAAACAGCGCGGTGAAACAGCGCTCTCCGTTATATAGAGCGCTTAGAA 87
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1 COUNTRY: U.S.
2 ZIP: 20036-5405
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: 3.25" Floppy Disk
5 COMPUTER: IBM PC Compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
7 SOFTWARE: IBM/Word Perfect 6.1 Windows
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/534,910B
10 FILING DATE: 28-SEPT-1995
11 CLASSIFICATION: 435
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: JP 7-25253
14 FILING DATE: 14-FEB-1995
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Toftenefti, Judith L.
17 REGISTRATION NUMBER: 39,048
18 REFERENCE/DOCKET NUMBER: 77670/398
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (202)429-1776
21 TELEFAX: (202)429-0796
22 INFORMATION FOR SEQ. ID NO: 1:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 894 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: double
27 TOPOLOGY: linear
28 MOLECULE TYPE: DNA
29 ORIGINAL SOURCE:
30 ORGANISM: Bacillus stearothermophilus
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QY 155 MetLeuAspMetGlnSerGluGlnProIleAspLeuGluThrLeuGluMetIleHis 174
DB 481 GCAGCCGATATGGAAGGAGAAACGCTGACGCTTCGAGCTGAAATACATTCAT 540
QY 175 LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsn 194
DB 541 CGGCATTAACCGGGAATATGCTGCATATACAGCGTGCACGCGCGCTTATCGCGCGC 600
QY 195 ValAspAspThrThrLysGluHisIleLeuGluSerTyrosThrHisLeuGluYmeMetThe 214
DB 601 GCTGATGCCCGGCAACGCGGAGCTTGCATTCGAAATTCGCGCCCATCTAGCGCTTGCCTTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrosGlyAspGluAlaLysLeuGlyLysLysVal 234
DB 661 CAATTCGCGATGATATTCCTCATATGTAGCGGCGAGAAAGAAATCGCAAGCGCTC 720
QY 235 GlySerAspLeuGluAsnAsnLysSerThrTyrosLysLeuLeuGlyLysAspGlyAla 254
DB 721 GCAGAGCAACCAAGCAACAACAAAGCGATCCAGCGCTGCTGCTGCTGCGCGCGC 780
QY 255 GluAspLysLeuThrTyrosHisArgAspAlaAla 265
DB 781 AAGGAAAGTTGCGCTTCATATCGAGCGCGC 813

RESULT 14

US-09-367-528A-2
Sequence 2, Application US/09367528A

Patent No. 635525
GENERAL INFORMATION:
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
TITLE OF INVENTION: Geranyl Diposphate Synthetase Gene
FILE REFERENCE: PH-586
CURRENT APPLICATION NUMBER: US/09/367,528A
PRIOR FILING DATE: 1999-08-15
CURRENT FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: JP97/346666
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 894
TYPE: DNA
ORGANISM: Bacillus stearothermophilus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(894)
US-09-367-528A-2

Alignment Scores:

Pred. No.: 4,43e-73 Length: 894
Score: 644.00 Matches: 133
Percent Similarity: 67.41% Conservative: 49
Best Local Similarity: 49.26% Mismatches: 86
Query Match: 44.32% Indels: 2
DB: 4 Gaps: 1

US-09-925-637-64 (1-287) x US-09-367-528A-2 (1-894)

QY 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25
DB 28 CTCACGACGCAAAACAGCGCGGTGGAACAGCGCTCTCCGTTATATAGCGCTTAGA 87
QY 26 MetAspThrGlnLeuGluGlnIleAspMetLeuTyrosSerLeuAsnAlaGlyLysArgIle 45
DB 88 GGGCCCGCGAAGCTGAAAAGCGATGCGTACTCATTTGGAGCGCGCGCAACGATC 147
QY 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrosGluLeuGlyMet 65
DB 148 GGTCCGTGCTGCTTCTGTCACCGTTCCGCGCGCTCGGCAAGAACCGCGCGGATTCG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrosSerLeuHisAspLeuPro 85
DB 208 CCCGTGCGCGCGATGAAATGATCATACGATCTTCTTGATTCATGATGATTTGCGC 267

QY 86 AlaMetAspAsnAspAspTyrosArgArgGlyLysLeuThrAsnHisLysValTyrosGlyGln 105
DB 268 AGCATGACACACATGATTTTCCGCGCGGCAACCGCAACCACTAAAGTTTCGCGCAG 327
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSer 124
DB 328 GCGATGCGCATCTTGGGGGAGCGAGGTTGTGACGTAACCGTTTCATATGATCACCAG 387
QY 125 ---SerAspAspArgLeuThrAspGluValLysIleLysValLeuGluAlaGlySerIle 143
DB 388 ATCGACGATGAGGCAATCCCTCTCCGTCGCGCTTCGCTCATCGAACCGCTGCGAAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlnMetLeuAspMetGlnSerGluGln 163
DB 448 GCGCGCGTCCGGAAGGATGTCGCGCGTCAAGCAGCATATGAGAGAGGAGAAA 507
QY 164 ProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThr 183
DB 508 ACGCTGACGCTTCGAGCTCGAATACATTCATCGGATTAACCGGAAATGCTGCAA 567
QY 184 PheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203
DB 568 TACAGCGTCAACCGCGCGCTTGATGCGCGCGCTGATCCCGGCAACGCGGAGCTT 627
QY 204 GluSerTyrosThrHisLeuGlyMetMetPheGlnIleLysAspAspLeuAspCys 223
DB 628 GACGATTCGCGCGCCCATCTAGGCTTGCCTTCAATTCGATATTCCTGATATT 687
QY 224 TyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsnAsnLysSer 243
DB 688 GAAGGGGCAAGAAATCGGCACACCGCTGCGCAGCAGCAACCAACCAACCAAGCG 747
QY 244 ThrTyrosLysLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrosArgAsp 263
DB 748 ACGTATCCAGCGTTGCTGCTGCTGCGCGCGCAAGAAAGTTGCGCTTCATATCGAG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
DB 808 GCGCGCAGCGCCATTTACGAAACGCCGAC 837

RESULT 15

US-09-275-742-1
Sequence 1, Application US/09275742

Patent No. 6130069
GENERAL INFORMATION:
APPLICANT: Wilding, Edwin Imogen
APPLICANT: Gwynn, Michael
TITLE OF INVENTION: Ispa
FILE REFERENCE: GM10205
CURRENT APPLICATION NUMBER: US/09/275,742
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 876
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-275-742-1

Alignment Scores:

Pred. No.: 3.72e-61 Length: 876
Score: 551.00 Matches: 122
Percent Similarity: 64.89% Conservative: 48
Best Local Similarity: 46.56% Mismatches: 88
Query Match: 37.92% Indels: 4
DB: 3 Gaps: 3

US-09-925-637-64 (1-287) x US-09-275-742-1 (1-876)

QY 28 ThrGlnLeuGluGlnIleAspMetLeuTyrosSerLeuAsnAlaGlyLysArgIleArgPro 47
DB 73 TCTAGTTACCGGAGTCTGTTCTCTATTCATATCATGCTGTGCAAGCGATTCGCGCT 132

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QY 48 ValLeuLeuLeuThrLeuAspSerLeuAsn---ThrGluTyrGluLeuGlyMetLys 66
Db 133 TTTCCTCTGTAAAGCTTCTGGAGGCTTGACAGTTTCCATCAAACTGCTCACGGCGAG 192
QY 67 SerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuProAla 86
Db 193 GTAGCTACTGCTTGAGATGATTCATACAGGAGCTGATTCACGATGACCTTCTGCT 252
QY 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGluTrp 106
Db 253 ATGGATGATGACATTATCGAAGAGGCGGTTTACCAATCACAGAAATTCGGTGAAGCT 312
QY 107 ThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSerAsp 126
Db 313 ATGGCCATTTTGGCTGGAGATGCTTATCTTATAGACCATATGCGCTTGATTCGCGAGGCA 372
QY 127 AspArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIleAlaSerGly 146
Db 373 GAT---TTGCCAAGTCAGATCAAGGCGGCTTGATGCCAAGCTTATCCTTCTCAGGT 429
QY 147 HisValGlyMetValGlyGlyMetLeuAspMetGlnSerGluGlnProIleAsp 166
Db 430 AGTCTGGGTATGTGGCAGGCGCAAGTTTGGATTTGGAGGCGCAACACGACCTTGCT 489
QY 167 LeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaVal 186
Db 490 CTGGAAAGACTTCAGACTATTCATGCCAATTAAGCTGGAGAGTACTAGCTATCCCTTC 549
QY 187 MetSerIleAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeuGluSerTyr 206
Db 550 CAAGCGGACGCTATTATAGCTGAATTGTCACTGAATGCAAGTGAAGCTGAAGAACTG 609
QY 207 SerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuAspCysTyrGlyAsp 226
Db 610 GGTGAATTGATGGACTTGCTTTTCAAGTCAGAGATGATGATCTGATGACGGCTAGT 669
QY 227 GluAlaLysLeuGlyLysLysValGlySerAspLeuGluAsnLysSerThrTyrVal 246
Db 670 TTGAGGAAATCGGCAAGACACCTCAAAAGGATCTGCGGCGAGAAAATCAACTATCCT 729
QY 247 SerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAspAlaAlaVal 266
Db 730 GCCTTGTTGGCTTGGAGAAGCTCATGCTTTTGTAAACCAACCTGGATCAAGCTAAT 789
QY 267 AspGluLeuThrGlnIleAspGluGln-----PheAsnThrLysHisLeuLeuGluIle 284
Db 790 GATAAATTAGAAATTTGCCAGACGACTTCCCTTTGAAACAGAAATGATGTTGAAGTGA 849
QY 285 ValAsp 286
Db 850 GTAGAA 855
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Search completed: April 20, 2004, 11:25:31
Job time : 77 secs

Tue Apr 20 12:43:40 2004

us-09-925-637-64.rnpb

Page 2

[illegible]

Db 841 TTATTAGAAATCGTTGATTTA 861

RESULT 2
US-10-084-205-63
/ Sequence 63, Application US/10084205
/ Publication No. US20030049648A1
/ GENERAL INFORMATION:
/ APPLICANT: Choi, G11
/ TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
/ FILE REFERENCE: PB515P1
/ CURRENT APPLICATION NUMBER: US/10/084,205
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: PCT/US00/23773
/ PRIOR FILING DATE: 2000-08-31
/ PRIOR APPLICATION NUMBER: 60/151,933
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: Patentin Ver. 3.1
/ SEQ ID NO 63
/ LENGTH: 861
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-084-205-63

Alignment Scores:
Pred. No.: 6,68e-162 Length: 861
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-925-637-64 (1-287) x US-10-084-205-63 (1-861)

QY 1 MetThrAsnLeuProMetAsnLysLeuTLeaSpGluValAsnAenGluLeuSerValAla 20
Db 1 ATATGCAATCTTACCGATGATTAATTAATTAAGTGAAGTCATTAATGATTCGGTTCGG 60
QY 21 IleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTyrSerLeuAsnAla 40
Db 61 ATAAATTAATCAAGTATGATGATCACTCAAGCTTAAGAAATGATATGTTGATTAATTAAGCT 120
QY 41 GlyGlyValArgGlyLeuArgProValLeuLeuLeuLeuLeuThrLeuAspSerLeuAsnTrpGlu 60
Db 121 GGAGGTAACGATCCGACCACTTCTGTTATTCTCACTTAAAGTTCACTTAATACCGAG 180
QY 61 TyrGluLeuGlyMetLysSerAsnAlaIleAlaLeuGluMetIleHisTrpTyrSerLeuIle 80
Db 181 TATAGATTAGATGATGAAGAGCCCAATTCACATGAAATGATTCATACATATTCACTATT 240
QY 81 HisAspAspLeuProIleMetAspAsnAspAspTyrArgArgGlyLysLeuTrpAsnHis 100
Db 241 CATATGACCTTACCAACCGATGATTAATGATGTTTTCACACAGAAATTAACAAATCAT 300
QY 101 LysValTyrGlyGluTrpThrAlaIleLeuAlaGlyAspAlaLeuLeuTrpLysAlaPhe 120
Db 301 AAAGTATATGATGATGAGCATCGATGATTTAGCAGGTGATGCTTTAATTAACTAAGCAATTT 360
QY 121 GluLeuLeuSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
Db 361 GAATCTTATTTCAAGTATGATGATTAATTAATCTAGATGAAGTAAATTAAGTTCTACACCG 420
QY 141 LeuSerIleLeuAspArgLysIleValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
Db 421 CTGTCATATGCAAGGTGATCATGTGAAATGTCGGCGGCTCAAAAGTTAGATGACCAAGC 480
QY 161 GluGlyValnProIleAspLeuGluTrpLeuGluMetIleHisLysTrpLysTrpGlyAla 180
Db 481 GAAGCGCAACCAATTGATCTTTGAACCTTTGGAAATGATACCAAAACAAAAACGAGACA 540
QY 181 LeuLeuThrTherAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLys 200
Db 541 TTATTAACTTTTCGGTATGATGATGAGACAGATATCGGTAAATGTCGATGATCAACTAAA 600

QY 201 GlnHisLeuGluSerThrYrSerThrHisLeuGlyMetMetPheGlnIleLeuAspAspLeu 220
 Db 601 GAACATTTAGAAATTTAGTATCATTTAGTATGATGTTCCAGATTAAGATGATTTA 660
 QY 221 LeuAspCysThrGlyAspGluAlaLeuGlyLysLysValGlySerAspLeuGluAsn 240
 Db 661 TTACACTGCTATGCTGATGAAGCAAAAGTTAGTAAAAAAGTGGCAGCATCTTGAATAA 720
 QY 241 AsnLysSerThrTrpValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTrp 260
 Db 721 AATAAAGTACGTCGAGGTTTATTAAGGAAAGATGCGCAGAGATTAATGACTTAT 780
 QY 261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
 Db 781 CATAGAGCGCAGCAGTGGATGAACCTAACGCAATTGATGACATTCATACAAAACAC 840
 QY 281 LeuLeuGluIleValAspLeu 287
 Db 841 TTATTAGAAATCGTTGATTTA 861

RESULT 3

US-08-781-986A-155/c
 ; Sequence 155, Application US/08781986A
 ; Publication No. US20030054436A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248BP

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 155:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1893 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

US-08-781-986A-155

Alignment Scores:

Pred. No.: 2,12e-161 Length: 1893
 Score: 1453.00 Matches: 287

Percent Similarity: 100.00% Conservatve: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-925-637-64 (1-287) x US-08-781-986A-155 (1-1893)

QY 1 MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
 Db 1314 ATGACGAAATCTACCCGATGAATTAATTAATAGATGAAGTCAATTAATGAATTAATCGGTTGG 1255
 QY 21 IleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuThrSerLeuAsnAla 40
 Db 1254 AATTAATTAATCGATATGATATCTACGCTAGAAAGATAGTTGATTCATTAATGCT 1195
 QY 41 GlyGlyLysArgLysArgProValLeuLeuLeuThrLeuAspSerLeuAsnThrGlu 60
 Db 1194 GAGGTTAAACGATCGACGACCACTCTGTTATTAACCACTTAATGATTAATACCGAG 1135
 QY 61 TrpGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTySerLeuIle 80
 Db 1134 TATGAGTTAGGTATGATGAAGCGCAATTCGATGAAAGATTCATACATTAATCACTTAT 1075
 QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTrpArgArgGlyLysLeuThrAsnHis 100
 Db 1074 CATGATGACCTTCCAGCGATGATTAATGATGATTCACAGCGAATAATTAACAATCAT 1015
 QY 101 LysValTrpGlyGluTrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
 Db 1014 AAAGTATATGATGAGTGGAGTCCGATATTAAGCAGGTGATGCTTTATTAATAACATTT 955
 QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
 Db 954 GAACCTTATTCAGATGATGATGATGATTAATCTGATGAAGTAAATTAATTAACCTTCAAC 895
 QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
 Db 894 CTGTCAATGACAAAGTGTATGTTGAAATGTCGCGCGGTCAATGTATGATATGCAAAAC 835
 QY 161 GluGlyGlnProIleAspLeuThrLeuGluMetIleHisLysThrLysThrGlyAla 180
 Db 834 GAAGGCCAACCAATGATCTTAACCTTGAAATGATACAAACAAACAAACAGAGCA 775
 QY 181 LeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrTrpLys 200
 Db 774 TTATTACTTTTGGCTTATGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 715
 QY 201 GlnHisLeuGluSerThrYrSerThrHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
 Db 714 GAACATTTAGAAAGTATATGATATCAATTAAGTATGATGATGATGATGATGATGATGAT 655
 QY 221 LeuAspCysThrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsn 240
 Db 654 TTAGACTGCTATGCTGATGATCAAGCAAAAGTTAGTAAAAAGTGGCAGCATCTTGAATAA 595
 QY 241 AsnLysSerThrTrpValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTrp 260
 Db 594 AATTAAGTACCTACCTGATGATTAATTAAGGAAAGTGGCGCAAGATTAATTAATGCTTAT 535
 QY 261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
 Db 534 CATAGAGCGCAGCACTGATGAACCAATTAATTAATTAATTAATTAATTAATTAATTAAT 475
 QY 281 LeuLeuGluIleValAspLeu 287
 Db 474 TTATTAGAAATCGTTGATTTA 454

RESULT 4

US-10-329-624-155/c
 ; Sequence 155, Application US/10329624
 ; Publication No. US20040043037A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-10-329-624-155

Alignment Scores:
Pred. No.: 2,12e-161 Length: 1893
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-329-624-155 (1-1893)

QY 1 MethrasleupPrometAenlyLeuileaspGluValasnsngileuservAlala 20
DB 1314 ATGACGAATCTACCGAATGAATTAATTAAGATGAATCAATATATGATTAATCGTTGGG 1255
QY 21 llaenlysservAlmetaspThngluengluiserwelleuTYrserleuaenAla 40
DB 1254 ATAATTAATCAGTAAGATGATACCTCAGCTAGAAAGATGTTGTTGTTTCAATTAATGCT 1195
QY 41 GllygllysaAgileatgProvalleuileuileuThreuasPserleuaenThnglu 60
DB 1194 GGAAGTAACCGATCCGACGCTTCTGTATTACTCTTAATTAATTAATTAATCCGAG 1135
QY 61 TyrgluenglyMetlysservAllealeuengluMetlleisthTYrserleuile 80
DB 1134 TATAGTAGGTATGAAGAAGCGCAATGCACTAGAAATGATTCAATCAATTAATCACTATT 1075
QY 81 HisaspaleupProalAmetaspasaspPtyrtaargtgglylyssleuthraenHs 100
DB 1074 CATGTAGCTTACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
QY 101 LysValTYrGlyGluTYrThrAlaIleuValaglyaspAlaleuileuThrysaIaPh 120
DB 1014 AAAGTAATGTGTGATGAGTGCATGATTAACAGCTGATGATGATTAATTAATTAACGATT 955
QY 121 GluLeuileSerSeraspaspargleuThraspGluVallystlelyValleuGlnarg 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-10-329-624-155

Alignment Scores:
Pred. No.: 2,12e-161 Length: 1893
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-329-624-155 (1-1893)

QY 1 MethrasleupPrometAenlyLeuileaspGluValasnsngileuservAlala 20
DB 1314 ATGACGAATCTACCGAATGAATTAATTAAGATGAATCAATATATGATTAATCGTTGGG 1255
QY 21 llaenlysservAlmetaspThngluengluiserwelleuTYrserleuaenAla 40
DB 1254 ATAATTAATCAGTAAGATGATACCTCAGCTAGAAAGATGTTGTTGTTTCAATTAATGCT 1195
QY 41 GllygllysaAgileatgProvalleuileuileuThreuasPserleuaenThnglu 60
DB 1194 GGAAGTAACCGATCCGACGCTTCTGTATTACTCTTAATTAATTAATTAATCCGAG 1135
QY 61 TyrgluenglyMetlysservAllealeuengluMetlleisthTYrserleuile 80
DB 1134 TATAGTAGGTATGAAGAAGCGCAATGCACTAGAAATGATTCAATCAATTAATCACTATT 1075
QY 81 HisaspaleupProalAmetaspasaspPtyrtaargtgglylyssleuthraenHs 100
DB 1074 CATGTAGCTTACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
QY 101 LysValTYrGlyGluTYrThrAlaIleuValaglyaspAlaleuileuThrysaIaPh 120
DB 1014 AAAGTAATGTGTGATGAGTGCATGATTAACAGCTGATGATGATTAATTAATTAACGATT 955
QY 121 GluLeuileSerSeraspaspargleuThraspGluVallystlelyValleuGlnarg 140

RESULT 5
US-10-282-122A-8179
Sequence 8179, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyuth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636

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/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PAM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 8179
/ LENGTH: 882
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-282-122A-8179

Alignment Scores:
Pred. No.: 8,02e-161 Length: 882
Score: 1444.00 Matches: 285
Percent Similarity: 99.65% Conservative: 1
Best Local Similarity: 99.30% Mismatches: 1
Query Match: 99.38% Indels: 0
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-282-122A-8179 (1-882)

QY 1 MetThrsAnLeuProMetAsnLysLeuLeaSpGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGACGAATCTTCCGATGCAATGAATTAATTAATGATGAATCAATTAATGATGCG 60
QY 21 IleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTySerLeuAsnAla 40
DB 61 ATAAATTAATTCAGTAATGATGATCTCAGCTAGAAGAAAGATGTTGATTCATTAAATCT 120
QY 41 GlyGlyValAspGlnLeuProValLeuLeuLeuLeuThLeuAspSerLeuAsnThrGlu 60
DB 121 GAGAGTAACGCAATCCGACCACTTCTGTATTAATCACTTGAATCACTTAATCCGAG 180
QY 61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTySerLeuIle 80
DB 181 TATGAGTATGAGTGTGAAGCGCAATTCAGTAAGTAATGATTCAGTCAATATCACTTAT 240
QY 81 HisAspAspLeuProLamMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHis 100
DB 241 CATGATGACCTACCGACGATGATGATGATGATTCGACGAGGAAATTAACAATATAT 300
QY 101 LysValTyGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
DB 301 AAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
DB 361 GAACATTAATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGluMetLeuAspMetGlnSer 160
DB 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 161 GluGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
DB 481 GAAGGCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 181 LeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLys 200
DB 541 TATTAATCTTTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 201 GluHisLeuGluSerTySerTyrHisLeuGluMetMetPheGlnIleLysAspAspLeu 220
DB 601 GAACATTTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 221 LeuAspCysTyGlyAspGluAlaLysLeuGluLysLysValGlySerAspLeuGlnSer 240
DB 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 241 AsnLysSerThrTyValSerLeuLeuGluLysAspGlyAlaGluAspLysLeuThrTy 260
DB 721 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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QY 261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
DB 781 CATGACGACCGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 281 LeuLeuGluIleValAspLeu 287
DB 841 TTATTAGAAATCGTTGATTTA 861

RESULT 6
US-09-815-242-8485
/ Sequence 8485, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zykkind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Treawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA, 011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8485
/ LENGTH: 882
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(882)
US-09-815-242-8485

Alignment Scores:
Pred. No.: 1.38e-160 Length: 882
Score: 1442.00 Matches: 285
Percent Similarity: 99.30% Conservative: 0
Best Local Similarity: 99.30% Mismatches: 2
Query Match: 99.24% Indels: 0
DB: 9 Gaps: 0

US-09-925-637-64 (1-287) x US-09-815-242-8485 (1-882)

QY 1 MetThrsAnLeuProMetAsnLysLeuLeaSpGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGACGAATCTTCCGATGCAATGAATTAATTAATGATGAATCAATTAATGATGCG 60
QY 21 IleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTySerLeuAsnAla 40
DB 61 ATAAATTAATTCAGTAATGATGATCTCAGCTAGAAGAAAGATGTTGATTCATTAAATCT 120
QY 41 GlyGlyValAspGlnLeuProValLeuLeuLeuLeuThLeuAspSerLeuAsnThrGlu 60
DB 121 GAGAGTAACGCAATCCGACCACTTCTGTATTAATCACTTGAATCACTTAATCCGAG 180
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PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4184
LENGTH: 864
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-815-242-4184

Alignment Scores:
Pred. No.:      2,09e-157      Length:      864
Score:          1415.00       Matches:     280
Percent Similarity: 99.22%    Conserved:   0
Best Local Similarity: 99.22%    Mismatches:  2
Query Match:    97.38%       Indels:      0
DB:             Gaps:        0

US-09-925-637-64 (1-287) x US-09-815-242-4184 (1-864)

Cy      6 MetAsnThLyLeuIlAASPGLVValAsmngInuSeRValAlAlleuNlyServal 25
Db      1 ATAAATTAATTATAGTAGTGAAGTCATAATGATTAACGGTGCGATTAATTAATCAGTA 60

Cy      26 MetAspThGlInLeuGIuISerMetLeuTyIseLeuAnaIGLyGlyIsArgIle 45
Db      61 ATGTGATACCACACTGGAAGAAGATGTGTGATTCATTAAATGCTGAGGTAACGCATC 120

Cy      46 ArgpCvAlleuLeuLeuLeuThrLeuAspSerLeuAnThrGluTyrgIuLeuGIYmet 65
Db      121 CGACCAAGTTCTGTATTACTCATCTTAATTCACATAAATACCGAGTATGAGTATG 180

Cy      66 LysSerAlAllealaleuGIuMetIleHsthTrYSerLeuIleHisaspLeuPro 85
Db      181 AAAGGGCAATTGCCCTGAAATGATTCATCATTCATTCATTCATGATGACCTACCA 240

Cy      86 AlameAspAsnaSPAsPTyrzArGArgGLyLysLeuthrAnhiSLyValTYrgLYGu 105
Db      241 GCAGTGGATTAAGATGATTAATGACGAGGGAATTAACAATCATTAAGATATAGTGAG 300

Cy      106 TrpThAlAlleuAlAGLyAspAlaLeuLeuThrYsaAPegIuSuIIeserSer 125

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QY	126	ASPAAPARGLIETHRASPGLIYVALLYSILEYVALLEUNGINARGLEUSERILEALSER	145
DB	361	GATGATAGATTACTGATCATAGTAAATAAGTTCTACACCGCTGTCAATGCAAGT	420
QY	146	GLYHLSVALGLYMETVALGLYGLYMETLEUASPHEGLINSERGLINGINPROILE	165
DB	421	GGTCATGTTGGAAATGGTGGCGCGTCMAATGTAGATAGCAACGGAAGCCAACTT	480
QY	166	ASPLEUGLITHTLEUGLIMETLEHLSYSTRHYSTRGVALALEUAEUTHRPHALA	185
DB	481	GACTTTGAAACTTTGGAAATGATTAACAAACAAACACGAGACATATTACATTTGGC	540
QY	186	VALMETSERVALALASPILLEALASVALASPAPTRHTHYLSGLIHLISLEUGLUSER	205
DB	541	GTTATAGTCGACGACGATATCCCTTAATGTCATGATGCAATTAAGAACAATTGGAAGT	600
QY	206	TYRSEPTYHISLEUGLYMETWEPHEGINLILEYASPAAPLEULEASPCTYRGLY	225
DB	601	TATAGTTATCATTTAGGTATGATGATTTCAAGCTTAAGATGATTTATTATGACTGGTAAAGT	660
QY	226	ASPGILVALILEUGLILYLYELVALGLYSEARSPLEUGIUAENASLYSERTHR	245
DB	661	GATGAAGCCAAAGTATGGTAAAAAGTGGCGACGACTTGAATAATTAATAAAGTACATAC	720

QY 246 ValSerLeuLeuGluGlyAspGlyValGluAspGlyLeuThrTyrHisArgAspAlaIala 265
Db 721 GGGAGATTATATGAGAAAGATGCGCAGAAAGATTAATTACTTATCATGAGACCGCAGCA 780
QY 266 ValAspGluLeuThrGlnIleAspGluGlnIlePheAsnThrLysHisLeuLeuGluIleVal 285
Db 781 GTGGATGAACCTAATGCAAAATTGATGAACATTCATCAACAAACACTTATTAGAAATCGTT 840

QY 286 AspLeu 287
Db 841 GATTTA 846

RESULT 8

US-10-282-122A-35068
Sequence 35068, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 35068
LENGTH: 879
TYPE: DNA
ORGANISM: *Staphylococcus haemolyticus*
US-10-282-122A-35068

Alignment Scores:

Pred. No.: 4,64e-113 Length: 879
Score: 1040.00 Matches: 18
Percent Similarity: 83.62% Conservative: 42
Best Local Similarity: 68.99% Mismatches: 47
Query Match: 71.58% Indels: 0
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-282-122A-35068 (1-879)

QY 1 MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnGluLeuSerValAla 20
Db 1 ATGGCAAAAGAAAGTCAAAAGAAATGAATTAAATCAAAATTAATAGCGCTTTGACGGTGA 60
QY 21 IleAsnLysSerValMetAspThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAla 40
Db 61 ATCGAAACTTCACACCTAATTAATGCAATCTTGAGAAAGATGCAATTTCTCTCAATGCG 120
QY 41 GlyGlyLysArgIleArgProValLeuLeuLeuLeuLeuAspSerLeuAsnThrGlu 60
Db 121 GTGGTAAAGAAATGAAGACCACTTCTGTATTTTAAACATTAGATGATTAATCAAGAT 180
QY 61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80
Db 181 TATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 240
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHis 100
Db 241 CATGATGATCTTCCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 101 LysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
Db 301 AAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
Db 361 GAATCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlnMetLeuAspMetGlnSer 160
Db 421 TTACGGCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 161 GluGlyGlnProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAla 180
Db 481 GAAGATTAACCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 181 LeuLeuThrPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLys 200
Db 541 TTACTTCATTCGAGATTAATGAAGCGAGCTGATGATGATGATGATGATGATGATGATG 600
QY 201 GluHisLeuGluSerTyrSerTyrHisLeuGluMetSerPheGlnIleLysAspAspLeu 220
Db 601 CAAAGCTTTGAAGATTTTAAGTAATCATATGAGGTTGATGATGATGATGATGATGATG 660
QY 221 LeuAspCysTyrGlyAspGluAlaLysLeuGlyLysLysValGlySerAspLeuGluAsn 240
Db 661 CTCGACGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyValGluAspLysLeuThrTyr 260
Db 721 CACAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 261 HisArgAspAlaIleValAspGluLeuThrGlnIleAspGluGlnIlePheAsnThrLys 280
Db 781 CATTAAGATGCTGCAAAAATCAATGAACAACTTCTTCACACATGATGATTAATAAAGCT 840

RESULT 9

US-10-282-122A-34531
Sequence 34531, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John

```

APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34531
LENGTH: 879
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34531

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Alignment Scores:

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Pred. No.: 4,19e-110      Length: 879
Score: 1015.00           Matches: 197
Percent Similarity: 82.93%      Conservative: 41
Best Local Similarity: 68.64%      Mismatches: 49
Query Match: 69.86%           Indels: 0
DB: 13                      Gaps: 0

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US-09-925-637-64 (1-287) x US-10-282-122A-34531 (1-879)

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QY 1 MetThraenleuprometasnlyleuileaspgluvalasnaengluLeuSerValala 20
DB 1 ATGAAGAAGACTACAGATGAAATTAATTAATAATTAATTAATACATCAGCAATTAAGTCA 60
QY 21 llaenlyserValmetaspThrglnleugluugetmetleuTySerleuAala 40
DB 61 ATACATCATCACCATTAAATTAATTAAGAAAGATGAAATTTACATTAAAGCT 120
QY 41 GluGlyLysArgileArgProValleuLeuLeuThraeApsSerleuAsthGlu 60
DB 121 CGGTGTAAGAAAGATGACGACGATCATATTAATTAACACATAAAAGCTTAACAAGAT 180
QY 61 TyGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHstHrTySerleuIle 80
DB 181 TATCAACAAGACTAAATATGCTTTAGCATTTGAAATGATTCATCTTATCTTAAAT 240
QY 81 HisAspAspLeuProAlaMetAspAsnAspAspTyArgArgGlyLysLeuThraShis 100
DB 241 CATGATGATTTCCGCAATGATGATTAACATTAACCTTAAGCAAAATTAACAATCAT 300
QY 101 LysValTyGlyGlyTyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThraIlePhe 120
DB 301 AAAGTTTATGATGAAAGCAATCTTCTGCTGATGATTAATTAACAAGCTTTT 360
QY 121 GluLeuIleSerSerAspAspArgLeuThraSpGluValLysIleValleuGlnArg 140

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DB 361 GAATTAAGTTTCATATGATACATACATGAGATAGTGGAAAGTATATATAAAACA 420
QY 141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSer 160
DB 421 CTTTCAAAAGCAAGGACATTTGGGAATGGGTGGCCCAAGCGCTGATATGAAAGT 480
QY 161 GluGlyGlnProIleAspLeuGluThraLeuGluMetIleHstLysThraLysThraIle 180
DB 481 GAAAGGAGTCAATTCGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
QY 181 LeuLeuThraPheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThraLys 200
DB 541 TTACTAAATTTTTCAGTATGCTGCGGTAGCATGTCATCAAGTAGAACAAATATGCT 600
QY 201 GluHstLeuGluSerTySerTyHstLeuGlyMetMetPheGlnIleLysAspAspLeu 220
DB 601 AAGAAATTAAGATGAAATTTAGCATCATTTAGCAATGATGCTTCAAAATTAAGATTAAT 660
QY 221 LeuAspCyTyGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsn 240
DB 661 CTGATGCTATGATGATGATGATCAAACTGGCAAAAAGTAGCAGATATTAATTAAT 720
QY 241 AsnLysSerThraTyValSerleuLeuGlyLysAspGlyValaGluAspLysLeuThraTy 260
DB 721 CATAAAGACTATTAATGTTCTTTACTTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 261 HisAspAspAlaAlaValaAspGluLeuThraGlnIleAspGluGlnPheAsnThraLysHis 280
DB 781 CATCAATATCTGCTATGAGACGCTTAATCAATATTCATCATATGATATGATCTGAA 840
QY 281 LeuLeuGluIleValaAspLeu 287
DB 841 TTAAGTATATGATGATTTA 861

RESULT 10
US-10-282-122A-24756
Sequence 24756, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

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/ PRIOR APPLICATION NUMBER: 60/269,308
 / PRIOR FILING DATE: 2001-02-16
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 78614
 / SOFTWARE: Patent version 3.1
 / SEQ ID NO: 24756
 / LENGTH: 882
 / TYPE: DNA
 / ORGANISM: *Listeria monocytogenes*
 / US-10-282-122A-24756

Alignment Scores:

Pred. No.:	3,73e-73	Length:	882
Score:	702.50	Matches:	148
Percent Similarity:	69.29%	Conservative:	46
Best Local Similarity:	52.86%	Mismatches:	81
Query Match:	48.35%	Indels:	5
DB:	13	Gaps:	2

US-09-925-637-64 (1-287) x US-10-282-122A-24756 (1-882)

QY 8 LysLeuileaspdluValasnngluLeuSerValAlaileasnlyseValMetasp 27
 DB 37 AAAGTATTGATGAG-----TCGCTTTTAAAGAAATTAACGACGAAATATCGAA 87
 QY 28 ThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAlaGlyGlyValArgIleArgPro 47
 DB 88 CCTAGACTAAAGAGTCATGTTATATCTTCAAGACGGGGGAAACGAGATTCGTCA 147
 QY 48 ValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluLeuGlyMetLysSer 67
 DB 148 ATGCTAGTTTTCGCTACGCTTCAAGCTTAAAGAAATCCGCTTTAGGTAAAC 207
 QY 68 AlaileAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuProAlaMet 87
 DB 208 GCAACGCGCTTGAATGATGATTCACACATACACCTTATTCAGATGATCCGCAATG 267
 QY 88 AspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyLutProThr 107
 DB 268 GATACGATGATTCGTCGAGGCAAGTGCATTAATGATTTGGCGATCAACT 327
 QY 108 AlaileLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSerAspAsp 127
 DB 328 GCGATTTTGGCAGAGATGCTTTACTTAACGCTCGCTTTTCTATTAGCTGACGAT 387
 QY 128 ArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIleAlaSerGlyHis 147
 DB 388 AATTATATCTTTGAGACACGATGCTTGAATTAACAAATTAAGTTAGTACGCTCA 447
 QY 148 ValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGlnProIleAspLeu 167
 DB 448 GAAGGATGTTGGTGGTCACTTGCAGACTTGAAGGGAACAAACAGATGACGTA 507
 QY 168 GlnThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaValMet 187
 DB 508 GAAGATTAATCATCATTCATGACGAAACAGGGTGAATTAATTAATTAAGCTGTAAC 567
 QY 188 SerAlaAlaAspIleAlaAsnValAspAspThrThrLysGlnHisLeuGlnSerTyrSer 207
 DB 568 TGTGACGCAAAATTCGCGAGCTGATCCAGAAACAAACGATTGCAATTTTCA 627
 QY 208 TyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuLeuAspCysTyrGlyAspGlu 227
 DB 628 GGAATTAATGAGATGATTTCAAAATTAAGCAGATTAATTAATTAAGTGGATAA 687
 QY 228 AlaLysLeuGlyLysLysValGlySerAspLeuGluAsnLysSerThrTyrValSer 247
 DB 688 AGGAAATGCTTAAGCAAGAGGCGGCGGCGCTTTTCGAAATTAAGTACCTATCCCGA 747
 QY 248 LeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAspAlaAlaValAsp 267
 DB 748 TTACTACGCTTGAATGCGGCAAAAGGCGATTAATTAAGTACGATTCGCAATGCA 807

QY 268 GluLeuThrGlnLeuAspGluGlnPheAsnThrLysHisLeuLeuGluIleValAspLeu 287
 DB 808 GCGCTTTCAGGCGATGAT-----TTGATGATGAATTCCTTGAACCTGCTGATTTA 861

RESULT 11

US-10-398-221-3823
 / Sequence 3823, Application US/10398221
 / Publication No. US20040018514A1
 / GENERAL INFORMATION:
 / APPLICANT: KUNST, Frederick
 / APPLICANT: GLASER, Philippe
 / TITLE OF INVENTION: *Listeria innocua*, genome and applications
 / FILE REFERENCE: 344 702 - US
 / CURRENT APPLICATION NUMBER: US/10/398,221
 / PRIOR FILING DATE: 2003-03-27
 / PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 / PRIOR FILING DATE: 2001-10-04
 / PRIOR APPLICATION NUMBER: FR 00/12 697
 / NUMBER OF SEQ ID NOS: 4025
 / SOFTWARE: Patent version 3.0
 / SEQ ID NO: 3823
 / LENGTH: 5635
 / TYPE: DNA
 / ORGANISM: *Listeria monocytogenes* 4b

FEATURE:

/ NAME/KEY: misc_feature
 / LOCATION: (1)..(end)
 / OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
 / US-10-398-221-3823

Alignment Scores:

Pred. No.:	3,79e-71	Length:	5635
Score:	695.50 <td>Matches:</td> <td>148 </td>	Matches:	148
Percent Similarity:	68.93% <td>Conservative:</td> <td>45 </td>	Conservative:	45
Best Local Similarity:	52.86% <td>Mismatches:</td> <td>82 </td>	Mismatches:	82
Query Match:	47.87% <td>Indels:</td> <td>5 </td>	Indels:	5
DB:	16 <td>Gaps:</td> <td>2 </td>	Gaps:	2

US-09-925-637-64 (1-287) x US-10-398-221-3823 (1-5635)

QY 8 LysLeuileaspdluValasnngluLeuSerValAlaileasnlyseValMetasp 27
 DB 2914 AAAGTATTGATGAG-----TCGCTTTTAAAGAAATTAACGACGCAAAATATCGAA 2964
 QY 28 ThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAlaGlyGlyValArgIleArgPro 47
 DB 2965 CCTAGACTAAAGAGTCATGTTATATCTTCAAGACGGGTGAATTAACGATTCGCC 3024
 QY 48 ValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluLeuGlyMetLysSer 67
 DB 3025 ATGCTAGTTTTCGCTACGCTTCAAGCTTAAAGTAAATCCGCTTTAGGTGGAACAA 3084
 QY 68 AlaileAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuProAlaMet 87
 DB 3085 GCAACGCGCTTGAATGATGATTCACACATACACCTTATTCAGATGATCCGCAATG 3144
 QY 88 AspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyLutProThr 107
 DB 3145 GATACGATGATTCGTCGAGGCAAGTGCATTAATGATTTGGCGATCAACT 3204
 QY 108 AlaileLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSerAspAsp 127
 DB 3205 GCAATTTTGGCAGAGATGCTTTACTTAACGCTCGCTTTTCTATTAGCTGACGAT 3264
 QY 128 ArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIleAlaSerGlyHis 147
 DB 3265 AATTATATCTTTGAGACACGATGCTTGAATTAACAAATTAAGTTAGTACGATGCA 3324
 QY 148 ValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGlnProIleAspLeu 167
 DB 3325 GAAGGATGTTGGTGGTCACTTGCAGACTTGAAGGGAACAAACAGATGACATTA 3384

QY 168 GluThrleuGluMetIleHisIysThrThrGlyAlaIleuLeuThrPheAlaValMet 187
DB 3385 GAAGAACTATCATCCATCCATGACGAGAAACAGCGCAATTATTAATTTTGGCGTAAC 3444
QY 188 SerAlaIleAspIleAlaAsnValAspAspThrThrIleGluHisIleuGluSerIysSer 207
DB 3445 TCTGCTCGCAAAATTCGAGAAGCTGACCCGGAACAAAGAAAGATTACGATTTTGGG 3504
QY 208 TyrHisIleuGluMetMetPheGlnIleIleAspAspIleuLeuAspCysIleGlyAspGlu 227
DB 3505 GAATAATTTGGAGATTGGATTCCCAATCGACGACATTTTATGATGTTATTTGGTGATGA 3564
QY 228 AlaIleuGluGlyIleValIleGlySerAspIleuGluAsnIleuIleSerThrIleValIleSer 247
DB 3565 ACAGAAATGGGTAAAGACAGCGGCTGACGCTTTCTGAAACAAAGTACCTATCCCGGA 3624
QY 248 LeuLeuGlyIleAspGlyAlaGluAspIleuThrIleIleArgAspAlaAlaValAsp 267
DB 3625 TTACTCAGCTTGTATGGTCCAAAGGCGCATTAATGAGCATGTTGCGATTGCAAAAGTCA 3684
QY 268 GluLeuThrGlnIleAspGluGlnPheAsnThrIleHisIleuLeuGluIleValIleAspGlu 287
DB 3685 GCGCTTCAGGCGCATGAT-----TTTGATGATGAATTTCTTTGAACACTTGCTGATTTA 3738

RESULT 12

US-09-815-242-2822/C
Sequence 2822, Application US/09815242
General Information:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2822
LENGTH: 413
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-815-242-2822

Alignment Scores:

Pred. No.: 3,698-72 Length: 413
Score: 690.00 Matches: 137
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.49% Indels: 0
DB: 9 Gaps: 0

US-09-925-637-64 (1-287) x US-09-815-242-2822 (1-413)

QY 54 LeuAspSerIleuAsnThrGluIleValIleuGluMetIleHisIleuGluMet 73
DB 413 TTAGATTACTTAATTAACCGAGTATGATGATGATGAAGCGGCAATTGCACTAGAAATG 354
QY 74 IleHisIleuGluMetIleHisIleuGluMetIleHisIleuGluMetIleHisIleuGluMet 93
DB 353 ATTCAATACATATTCATCTTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 294
QY 94 ArgGlyIleuLeuThrAsnHisIleuValIleuGluIleuThrAlaIleuLeuGluVal 113
DB 233 CGAGGAAATTAATTAACCAATCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 234
QY 114 AlaLeuLeuThrIleValIleuGluIleuSerIleuAspAspArgLeuThrAspGluVal 133
DB 233 GCTTATTAATTAATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 174
QY 134 IysIleuValIleuGluIleuSerIleuAspAspArgLeuThrAspGluValIleuGluVal 153
DB 173 AAAATTAATTAATTAACCAATCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 114
QY 154 GlnMetIleuAspMetGlnSerGluGluIleuPheIleuGluIleuThrIleuGluMetIle 173
DB 113 CAAATGTTAGATATGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 54

RESULT 13

US-10-282-122A-5390/C
Sequence 5390, Application US/10282122A
General Information:
APPLICANT: Wang, Lianggu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forey, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 5390
/ LENGTH: 413
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-282-122A-5390

Alignment Scores:

Pred. No.: 3,696-72 Length: 413
Score: 690.00 Matches: 137
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.49% Indels: 0
DB: 13 Gaps: 0

US-09-925-637-64 (1-287) x US-10-282-122A-5390 (1-413)

QY 54 LeuApsSerLeuAenThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMet 73
DB 413 TTAGATTCTCAATAACGAGATAGATTAGATGAAGGCAATTGCACTGAATG 354
QY 74 ILeHSTTrTyrSerLeuIleHisAspAspLeuProAlaMetAspAspAspTyrArg 93
DB 353 ATTCTATACATATCTTATTCATGATGACCTACCGAGATGATATGATGATATGCA 294
QY 94 AcGGAlYLySLeuThrAspHisLysValTyrGlyGluTTPThrAlaIleLeuAlaGlyAsp 113
DB 293 CGAGGAATTTACAAATCATATAAGTATATGCTGAGTGCATCTGCATATTGCGAGTAT 234
QY 114 AlaLeuLeuThrLysAlaPheGluLeuIleSerSerAspAspArgLeuThrAspGluVal 133
DB 233 GCTTATATTACAAAGCATTTGACTTATTCATGATGATGATGATGATGATGATGAT 174
QY 134 LysIleValLeuGluArgSerLeuIleAspSerGlyHisValGlyMetValGly 153
DB 173 AAAATTAAGTTCTCAACGGCTGTCAATAGCAAGTGGTCATGTTGGAATGGTGGCGGT 114
QY 154 GlnMetLeuAspMetGlnSerGluGlnProIleAspLeuGluThrLeuGluMetIle 173
DB 113 CAATGTTTGAATATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 54
QY 174 HisLysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIle 190
DB 53 CCAAAACAAAACAGGAGCATTTAATCTTTGGGTTATGAGTCAGCA 3

RESULT 14

US-10-398-221-8/c
/ Sequence 8, Application US/10398221
/ Publication No. US20040018514A1
/ GENERAL INFORMATION:
/ APPLICANT: KUNST, Frederik
/ APPLICANT: GLASER, Philippe
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 - US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ PRIOR FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: FR 00/12 697
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 8
/ LENGTH: 495269
/ TYPE: DNA
/ ORGANISM: Listeria innocua
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(end)
/ OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-8

Alignment Scores:

Pred. No.: 3,096-67 Length: 495269

Score: 686.50 Matches: 146
Percent Similarity: 68.21% Conservative: 45
Best Local Similarity: 52.14% Mismatches: 84
Query Match: 47.25% Indels: 5
DB: 16 Gaps: 2

US-09-925-637-64 (1-287) x US-10-398-221-8 (1-495269)

QY 8 LysLeuIleAspGluValAsnGlnLeuSerValAlaIleAsnLysSerValMetAsp 27
DB 366194 AAAGTACTGATGAG-----TCGCTTTTAAAGAAATAAATATGCGCAATATCGAA 366144
QY 28 ThrGlnLeuGlnGlnSerMetLeuTyrSerLeuAsnAlaGlyValLysArgIleAspPro 47
DB 366143 CTTAAGTTGAAGAAATCATATTTATTTATTCAGTCGAAGCTGGCGGAAACGAATTCCGTC 366084
QY 48 ValLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluLeuGlyMetLysSer 67
DB 366083 ATGCTTGTTTTTCACACGCTTCAACGCTTAATATATGAGCCAAATGCCGCTTTAAACAA 366024
QY 68 AlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuProAlaMet 87
DB 366023 GCTACGCACTGAAATGATATCATATGATGATGATGATGATGATGATGATGATGATG 365964
QY 88 AspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGluTTPThr 107
DB 365963 GATGATGATGATCTATGACCGCGGAAATGAGCAACCAATTAATATATGCGTATGCAACA 365904
QY 108 AlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSerAspAsp 127
DB 365903 GCAATTTTACACGAGATGCTTTGTTTACACTGCTTTTCTATTAGTGAAGATGAA 365844
QY 128 ArgLeuThrAspGluValLysIleLysValLeuGluArgSerLeuIleAspSerGlyHis 147
DB 365843 AATCTATCTTTCGAAACGCGATTTGCTTATTAATTAACAAATTTGTTATGACATGAGCA 365784
QY 148 ValGlyMetValGlyGlnMetLeuAspMetGlnSerGluGlnProIleAspLeu 167
DB 365783 GAAGGATGAGTATGAGTGGCAACAAGCCGATATGAAAGCTGAAATTAACAAGTCACTTA 365724
QY 168 GlnThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaValMet 187
DB 365723 GAAGAAATTACCAATTCACGCTCGCAAACTGCGAATTAATTTTTCGAGTAACC 365664
QY 188 SerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeuGlnSerTyrSer 207
DB 365663 TCAGCGCAAAAATTCGCTGAAGCAACTCCAGAACAAACAAACGATTACGAATTTTTCGA 365604
QY 208 TyrHisLeuGlyMetLysPheGlnIleLysAspAspLeuAspAspTyrGlyAspGlu 227
DB 365603 GAAATATTCGGATGCTGTTTCAAAATTAAGGAGCAATTTTAAGATGATTAATTCGCGATGA 365544
QY 228 AlaLysLeuGlyLysLysValGlySerAspLeuGluAsnAsnLysSerThrTyrValSer 247
DB 365543 ACATAAATGCTTAATAAAGAGGAGGTCGACGCTTCTGATTAATAAGTACTATCCCGGA 365484
QY 248 LeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAspAlaAlaValAsp 267
DB 365483 TTACTCACCTCGAAGGTGTAAACGGCATTAAATGAGCATTTTCAATTTGCAAAAGTCA 365424
QY 268 GlnLeuThrGlnLeuAspGlnPheAsnThrLysHisLeuGlnGluValAspLeu 287
DB 365423 GCGCTTCAAGACATGAT-----TTGACGATGAATTTCTCTTAACCTGCTGATTTA 365370

RESULT 15

US-10-398-221-2058
/ Sequence 2058, Application US/10398221
/ Publication No. US20040018514A1
/ GENERAL INFORMATION:
/ APPLICANT: KUNST, Frederik
/ APPLICANT: GLASER, Philippe
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 - US

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2004, 15:43:47 ; Search time 23 Seconds

(without alignments)
644,202 Million cell updates/sec

Title: US-09-925-637-64

Sequence: 1 MTNLPNNKLIDEVNNELSLVA.....ELTQIDQFNTHLEITDL 287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1436	98.8	293	3	US-09-276-873-2
2	1015	69.9	302	4	US-09-134-001C-3171
3	657	45.2	297	1	US-08-534-910B-9
4	654	45.0	297	3	US-08-886-466-2
5	654	45.0	297	3	US-09-475-304-2
6	654	45.0	297	4	US-09-101-126-3
7	653	44.9	297	4	US-08-534-910B-7
8	650	44.7	297	1	US-08-534-910B-8
9	650	44.7	297	1	US-08-534-910B-10
10	650	44.7	297	4	US-09-367-528A-5
11	646	44.5	297	4	US-09-367-528A-1
12	645	44.4	297	4	US-08-534-910B-6
13	644	44.3	297	4	US-09-367-528A-3
14	551	37.9	312	4	US-09-275-742-2
15	533	36.7	321	4	US-09-107-532A-6724
16	521	35.9	393	3	US-09-187-050-34
17	520.5	35.8	393	3	US-09-187-050-2
18	520.5	35.8	393	3	US-09-187-050-14
19	520.5	35.8	393	3	US-09-187-050-16
20	520.5	35.8	393	3	US-09-187-050-18
21	520.5	35.8	393	3	US-09-187-050-20
22	520.5	35.8	393	3	US-09-187-050-22
23	520.5	35.8	393	3	US-09-187-050-24
24	520.5	35.8	393	3	US-09-187-050-26
25	520.5	35.8	393	3	US-09-187-050-27
26	520.5	35.8	393	3	US-09-187-050-28
27	520.5	35.8	393	3	US-09-187-050-29

28	520.5	35.8	393	3	US-09-187-050-30	Sequence 30, Appl
29	520.5	35.8	393	3	US-09-187-050-31	Sequence 31, Appl
30	520.5	35.8	393	3	US-09-187-050-32	Sequence 32, Appl
31	520.5	35.8	393	3	US-09-187-050-33	Sequence 33, Appl
32	517	35.6	285	3	US-09-187-050-12	Sequence 12, Appl
33	516.5	35.5	297	4	US-09-934-903-14	Sequence 14, Appl
34	482	33.2	307	4	US-09-543-681A-5908	Sequence 5908, Ap
35	481	33.1	342	4	US-09-540-236-2612	Sequence 2612, Ap
36	480.5	33.1	299	4	US-09-469-039A-12733	Sequence 12733, A
37	480	33.0	280	4	US-09-634-238-303	Sequence 303, App
38	474.5	32.7	401	4	US-09-252-991A-26387	Sequence 26387, A
39	465.5	32.0	377	4	US-09-420-211-2	Sequence 2, Appl1
40	442	30.4	308	4	US-09-328-352-4190	Sequence 4190, Ap
41	376.5	25.9	302	1	US-07-783-705A-1	Sequence 1, Appl1
42	346	23.8	298	1	US-08-095-726-4	Sequence 4, Appl1
43	346	23.8	298	1	US-08-086-043-4	Sequence 4, Appl1
44	346	23.8	298	1	US-08-093-577-4	Sequence 4, Appl1
45	346	23.8	298	1	US-08-096-623A-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-276-873-2
; Sequence 2, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwina Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: Ispa
; FILE REFERENCE: GML0208
; CURRENT APPLICATION NUMBER: US/09/276, 873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-276-873-2

Query Match 98.8%; Score 1436; DB 3; Length 293;
Best Local Similarity 99.0%; Pred. No. 7.9e-135;
Matches 284; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MTNLPNNKLIDEVNNELSLVAINKSVMDTOLEESMTSLNAGKRIKRPVLLLTLDLSINTE	60
DB	1	MTNLPNNKLIDEVNNELSLVAINKSVMDTOLEESMTSLNAGKRIKRPVLLLTLDLSINTE	60
QY	61	YELGKSAIALEMHTHTSLIHDDLPANDNDYRRGKLTNKKYGEWTAIIAGALLTKAF	120
DB	61	YELGKSAIALEMHTHTSLIHDDLPANDNDYRRGKLTNKKYGEWTAIIAGALLTKAF	120
QY	121	ELISSDRILDEVYIKTLQRLSLASGHVGVGQMLDMQSEGPIDLETLEMIHKTGTGA	180
DB	121	ELISSDRILDEVYIKTLQRLSLASGHVGVGQMLDMQSEGPIDLETLEMIHKTGTGA	180
QY	181	LITFAVNSADIANVDDTYEHLSESYTHLGMFOIKODILLDCYGEBAKTKKYGSPLEN	240
DB	181	LITFAVNSADIANVDDTYEHLSESYTHLGMFOIKODILLDCYGEBAKTKKYGSPLEN	240
QY	241	NKSTFYVLLIGDGAEDKLTTHRDAVDELQIDQFNTKHLLEITDL 287	
DB	241	NKSTFYVLLIGDGAEDKLTTHRDAVDELQIDQFNTKHLLEITDL 287	
RESULT 2			
US-09-134-001C-3171			
; Sequence 3171, Application US/09134001C			
; Patent No. 6380370			
; GENERAL INFORMATION:			
; APPLICANT: Lynn Doucette-Stamm et al			

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3171
LENGTH: 302
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3171

Query Match 69.9%; Score 1015; DB 4; Length 302;
Best Local Similarity 68.6%; Pred. No. 6.5e-93;
Matches 197; Conservative 41; Mismatches 49; Indels 0; Gaps 0;

QY 1 MTNLPNNKLTIDEVNNELSVAINKSVMDTLEESYLYSLNAGKRIKIRPVLLLTLDSTLNT 60
DB 10 MKKLQNNKLTININTSINKSIQSSPLKTNLEESWKYSLNAGKRIKIRPVLLLTLDSTLNT 69
QY 61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRGGKLTNNKVTGEMTALLAGDALLTKAF 120
DB 70 YQGGINSKALEMHTYSLIHDDLPAMDNDYRGGKLTNNKVTGEMTALLAGDALLTKAF 129
QY 121 ELISSDRLTDEVKIKYLRSLASGHVGVGQMLDMOSEGQPIDLETLEMTIKTKTA 180
DB 130 ELVNDTTEISVAVSIIRKLSKASGHLGVGQALMESEKSIKLETLEMTIKTKTA 189
QY 181 LITAVMSADIANVDTTKEHLESYSYHGMFQIKODLLDCYGEBAKIGKVGSDLEN 240
DB 190 LITAVMSADIANVDTTKEHLESYSYHGMFQIKODLLDCYGEBAKIGKVGSDLEN 249
QY 241 NKSTYVSLGKDGAEKLTTHRDAAVDELQIDSEFTKHLLETVLD 287
DB 250 HKSTYVSLGKDGAEKLTTHRDAAVDELQIDSEFTKHLLETVLD 296

RESULT 3
US-08-534-910B-9
Sequence 9, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBARA, Shuhei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyozi
APPLICANT: KOYAMA, Taneoshi
TITLE OF INVENTION: Mutated fatty acid synthase capable
TITLE OF INVENTION: Of synthesizing geranylgeranyldiphosphate and gene coding therefor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofigenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-9

Query Match 45.2%; Score 657; DB 1; Length 297;
Best Local Similarity 47.7%; Pred. No. 2.7e-57;
Matches 133; Conservative 57; Mismatches 83; Indels 6; Gaps 2;

QY 1 MTNLPNNKLTIDEVNNELSVAINKSVMDTLEESYLYSLNAGKRIKIRPVLLLTLDSTLNT 56
DB 1 MAQSVQEPNEKQAVETALSRYTELEGKAKKMAVSLKAGKRIKIRPVLLLTSTVRA 60
QY 57 INTEYELGKSAIALEMHTYSLIHDDLPAMDNDYRGGKLTNNKVTGEMTALLAGDALL 116
DB 61 LKQDPVAGIPVACALEMHTYSLIHDDLPAMDNDYRGGKLTNNKVTGEMTALLAGDALL 120
QY 117 TPAEELIS--SDPRLTDEVKIKYLRSLASGHVGVGQMLDMOSEGQPIDLETLEMTIKTKTA 174
DB 121 TPAEELIS--SDPRLTDEVKIKYLRSLASGHVGVGQMLDMOSEGQPIDLETLEMTIKTKTA 180
QY 175 KTKTGALLTFAVMSADIANVDTTKEHLESYSYHGMFQIKODLLDCYGEBAKIGKVGSDLEN 234
DB 181 RHKTGKMLQYSHAGALLGADARQTRLEDEFAALGAFQIRDDIIDEAGEEKIGKRV 240
QY 235 GSDLENKSTYVSLGKDGAEKLTTHRDAAVDELQID 273
DB 241 GSDLENKSTYVSLGKDGAEKLTTHRDAAVDELQID 279

RESULT 4
US-08-886-466-2
Sequence 2, Application US/08886466C
Patent No. 6040165
GENERAL INFORMATION:
APPLICANT: NARITA, Keisshi
APPLICANT: ICHIDA, Chika
APPLICANT: TAKEUCHI, Yoshie
APPLICANT: OHNO, Shikara
APPLICANT: MISHINO, Tokuzo
TITLE OF INVENTION: MUTANT PRANIL DIPHOSPHATE SYNTHASE
FILE REFERENCE: 77670/494
CURRENT APPLICATION NUMBER: US/08/886,466C
CURRENT FILING DATE: 1997-07-10
EARLIER APPLICATION NUMBER: JP 8-191635
EARLIER FILING DATE: 1996-07-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-08-886-466-2

Query Match 45.0%; Score 654; DB 3; Length 297;
Best Local Similarity 47.7%; Pred. No. 5.3e-57;
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

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QY      1 MTNLPMNKLIDEVNNELSVAINKSVM----DTQLEESMLYSINAGGRIRPVLLLTLDLS 56
      1 MAOLSVGEQFLNEKQAVETALSRVIERLGRPAKLRKMAVSLGAGGRIRPRLTLSTVRA 60
      57 LNTVEYELGKMSALALEMHTYSLIHDDLPMANDNDYRSGKLTNNKYVGEWTAIILAGDALL 116
      61 LGKDPVAVGVPVACALIMHTYSLIHDDLPSMDNDLRRCKPTNNKVFGEWMAIILAGDGLL 120
      117 TKAFELIS--SDRLTDEVKIKVLRSLASGHVGVGGMMDMOSGQPIDLETLEMTH 174
      121 TYAFQILTEIDRIPPSVRLRIERLAKAAGEGVAVGQADMEGEGKTLTISELEYIH 180
      175 KKTGALLTFVAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKRV 234
      181 RHKTGKMLQYSVHAGALIGADARQRELDPEFAHGLAFQIRDDIILDIGAEEKIGKPV 240
      235 GSDLENNKSTYVSLGKQGAEDKLTYHRDAVDELTOID 273
      241 GSDOSNNKATYYPALLSLAGAKEXLAFHIEAQRHLNAD 279

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RESULT 5

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US-09-475-304-2
; Sequence 2, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keisshi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohts, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; CURRENT FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-475-304-2

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Query Match      45.0%; Score 654; DB 3; Length 297;
Best Local Similarity 47.7%; Pred. No. 5.3e-57;
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

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QY      1 MTNLPMNKLIDEVNNELSVAINKSVM----DTQLEESMLYSINAGGRIRPVLLLTLDLS 56
      1 MAOLSVGEQFLNEKQAVETALSRVIERLGRPAKLRKMAVSLGAGGRIRPRLTLSTVRA 60
      57 LNTVEYELGKMSALALEMHTYSLIHDDLPMANDNDYRSGKLTNNKYVGEWTAIILAGDALL 116
      61 LGKDPVAVGVPVACALIMHTYSLIHDDLPSMDNDLRRCKPTNNKVFGEWMAIILAGDGLL 120
      117 TKAFELIS--SDRLTDEVKIKVLRSLASGHVGVGGMMDMOSGQPIDLETLEMTH 174
      121 TYAFQILTEIDRIPPSVRLRIERLAKAAGEGVAVGQADMEGEGKTLTISELEYIH 180
      175 KKTGALLTFVAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKRV 234
      181 RHKTGKMLQYSVHAGALIGADARQRELDPEFAHGLAFQIRDDIILDIGAEEKIGKPV 240
      235 GSDLENNKSTYVSLGKQGAEDKLTYHRDAVDELTOID 273
      241 GSDOSNNKATYYPALLSLAGAKEXLAFHIEAQRHLNAD 279

```

RESULT 6

US-09-101-126-3

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; Sequence 3, Application US/09101126
; Patent No. 6316216
; GENERAL INFORMATION:
; APPLICANT: OHTO, CHIKARA
; APPLICANT: NAKANE, HIROYUKI
; APPLICANT: NISHINO, TOKUZO
; APPLICANT: OHNUMA, SHINICHI
; APPLICANT: HIROOKA, KAZUTAKE
; TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
; FILE REFERENCE: 77670/566
; CURRENT APPLICATION NUMBER: US/09/101,126
; CURRENT FILING DATE: 1999-04-27
; EARLIER APPLICATION NUMBER: PCT/JP97/03921
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: JP 8-307506
; EARLIER FILING DATE: 1996-11-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; OTHER INFORMATION: 86-92 is an Asp-rich domain
US-09-101-126-3

```

```

Query Match      45.0%; Score 654; DB 4; Length 297;
Best Local Similarity 47.7%; Pred. No. 5.3e-57;
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

```

```

QY      1 MTNLPMNKLIDEVNNELSVAINKSVM----DTQLEESMLYSINAGGRIRPVLLLTLDLS 56
      1 MAOLSVGEQFLNEKQAVETALSRVIERLGRPAKLRKMAVSLGAGGRIRPRLTLSTVRA 60
      57 LNTVEYELGKMSALALEMHTYSLIHDDLPMANDNDYRSGKLTNNKYVGEWTAIILAGDALL 116
      61 LGKDPVAVGVPVACALIMHTYSLIHDDLPSMDNDLRRCKPTNNKVFGEWMAIILAGDGLL 120
      117 TKAFELIS--SDRLTDEVKIKVLRSLASGHVGVGGMMDMOSGQPIDLETLEMTH 174
      121 TYAFQILTEIDRIPPSVRLRIERLAKAAGEGVAVGQADMEGEGKTLTISELEYIH 180
      175 KKTGALLTFVAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKRV 234
      181 RHKTGKMLQYSVHAGALIGADARQRELDPEFAHGLAFQIRDDIILDIGAEEKIGKPV 240
      235 GSDLENNKSTYVSLGKQGAEDKLTYHRDAVDELTOID 273
      241 GSDOSNNKATYYPALLSLAGAKEXLAFHIEAQRHLNAD 279

```

RESULT 7

```

US-08-534-910B-7
; Sequence 7, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyocho
; APPLICANT: KOYAMA, Taneoshi
; TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
; OF SYNTHESIZING GERANYLGERANYLDIPHOSPHATE AND GENE CODING THE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-7

Query Match 44.9%; Score 653; DB 1; Length 297;
Best Local Similarity 47.3%; Pred. No. 6.7e-57;
Matches 132; Conservative 56; Mismatches 85; Indels 6; Gaps 2;
QY 1 MTNLPNKLIDVENNELSVAINKSVM---DTOLEESMLYSLNAGGKRIKRPVLLITLSDS 56
DB 1 MAQSVSEQFLNEQKQAVETALSRYTEERLEGPAKVKKMAVSLKGGKRIKRPVLLITLSTVQA 60
QY 57 INTEVELKMSKALALEMHTYSLIHDDLPAFNDNDYRSGKLTNNKYVGWTAIIAGDALL 116
DB 61 LGKDPVAGLPVACALMHTYSLIHDDLPSMNDNDLRGKPTNNKYVPGMAIILAGDGL 120
QY 117 TKAFELIS--SDRLTDEVKIKVLRSLASGHVGVGGQMLDMQSGQPIDETLEMTIH 174
DB 121 TYAFQILTEIDDERIPPSVRLRLIERLAKAAGPEGMAVAGQADMEGEGKTLTISELEYIH 180
QY 175 KTKTGALLTFPAVMSAADIANVDITTEHLESYSLGMMFOIKDLDLCYGDEAKLGKVV 234
DB 181 RHKTGKMLQYVHAQALIGADARQTRLEDEFPAHLGLAFQIRDDIIDIEGAEKIGKPV 240
QY 235 GSDLENNKSTYVSLGKQGAEDKLTYPHDAVDELTOID 273
DB 241 GSDQSNKATYFALLSLAGAKKELAFHTEAQRHLRND 279

RESULT 8
US-08-534-910B-8
Sequence 8, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tanetsoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington

STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-8

Query Match 44.7%; Score 650; DB 1; Length 297;
Best Local Similarity 47.3%; Pred. No. 1.3e-56;
Matches 132; Conservative 55; Mismatches 86; Indels 6; Gaps 2;
QY 1 MTNLPNKLIDVENNELSVAINKSVM---DTOLEESMLYSLNAGGKRIKRPVLLITLSDS 56
DB 1 MAQSVSEQFLNEQKQAVETALSRYTEERLEGPAKVKKMAVSLKGGKRIKRPVLLITLSTVQA 60
QY 57 INTEVELKMSKALALEMHTYSLIHDDLPAFNDNDYRSGKLTNNKYVGWTAIIAGDALL 116
DB 61 LGKDPVAGLPVACALMHTYSLIHDDLPSMNDNDLRGKPTNNKYVPGMAIILAGDGL 120
QY 117 TKAFELIS--SDRLTDEVKIKVLRSLASGHVGVGGQMLDMQSGQPIDETLEMTIH 174
DB 121 TYAFQILTEIDDERIPPSVRLRLIERLAKAAGPEGMAVAGQADMEGEGKTLTISELEYIH 180
QY 175 KTKTGALLTFPAVMSAADIANVDITTEHLESYSLGMMFOIKDLDLCYGDEAKLGKVV 234
DB 181 RHKTGKMLQYVHAQALIGADARQTRLEDEFPAHLGLAFQIRDDIIDIEGAEKIGKPV 240
QY 235 GSDLENNKSTYVSLGKQGAEDKLTYPHDAVDELTOID 273
DB 241 GSDQSNKATYFALLSLAGAKKELAFHTEAQRHLRND 279

RESULT 9
US-08-534-910B-10
Sequence 10, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tanetsoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding Ther
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington

```

/ ADDRESSER: Kenyon & Kenyon
/ STREET: 1025 Connecticut Avenue, N.W., Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: U.S.
/ ZIP: 20036-5405
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.25" Floppy Disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
/ SOFTWARE: IBM/Word Perfect 6.1 Windows
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/534,910B
/ FILING DATE: 28-SEPT-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 7-25253
/ FILING DATE: 14-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Toifenetti, Judith L.
/ REGISTRATION NUMBER: 39,048
/ REFERENCE/DOCKET NUMBER: 77670/398
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)429-1776
/ TELEFAX: (202)429-0796
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 297 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Bacillus stearothermophilus
/ US-08-534-910B-10

```

```

Query Match      44.7%; Score 650; DB 1; Length 297;
Best Local Similarity 47.3%; Pred. No. 1.3e-56;
Matches 132; Conservative 55; Mismatches 86; Indels 6; Gaps 2;

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QY 1 MNLPLNKLIDEVNNELSVAINKSVN---DTQLEBSMKYSINAGGKRIRPVLLLTLDLSLNTVEYELGM 56
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1 MAQLSEQPLNEQKQAVETALSRYSIERLEGPAKKKAAVSLGAGKRIRPVLLLTSTVOA 60
QY 57 LNTVEYELGKSAIALEMHITYSLIHDDLPAMNDYRSGKLNNHKYVGEMTALLAGDALTLTAFAELIS- 116
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 61 LKQDPVAGIPVACALIMHITYSLIHDDLPAMDNDLRKGPNNHKVFGEMAILLAGDGLL 120
QY 117 TYAFELIS--SDRLTDEVKIKYLRSLASGHVGVGQMLDMQSEGPIDLETLEMTH 174
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 121 TYAFQILITIDDERIPPSVRLRIERLAKAAGPEGVAGQAADMEGEGKTLTSLSEYTH 180
QY 175 KTRTGALLTFAYMSADIANDVDTTKEHLESYSYHIGMMFOIKDILLDCYGEAKLGRKVGSDLENKKS 234
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 181 RKRITGMLQYSHAGLIGADARQREIDEPFAHLGLAFQIRDDILIDEGAEKIGKRPV 240
QY 235 GSDLENKKSITYVSLGKQGAEDKLTYYHRDAVDELTOID 273
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 241 GSDQSNKATVPALLSLAGAKKELAFHIAQRLRNAD 279

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```

RESULT 10
US-09-367-528A-5
/ Sequence 5, Application US/09367528A
/ Patent No. 6395525
/ GENERAL INFORMATION:
/ APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
/ TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
/ FILE REFERENCE: PH-586
/ CURRENT APPLICATION NUMBER: US/09/367,528A
/ PRIOR FILING DATE: 1999-08-16
/ PRIOR APPLICATION NUMBER: JP97/346686
/ PRIOR FILING DATE: 1997-12-16
/ NUMBER OF SEQ ID NOS: 6

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/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 297
/ TYPE: PRT
/ ORGANISM: Bacillus stearothermophilus
/ US-09-367-528A-5

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Query Match      44.7%; Score 650; DB 4; Length 297;
Best Local Similarity 49.6%; Pred. No. 1.3e-56;
Matches 134; Conservative 49; Mismatches 85; Indels 2; Gaps 1;

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QY 6 MNLKLIDEVNNELSVAINKSVMDTQLEBSMKYSINAGGKRIRPVLLLTLDLSLNTVEYELGM 65
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 10 LNEQKQAVETALSRYSIERLEGPAKKKAAVSLGAGKRIRPVLLLTSTVRLGKDPVAVGL 69
QY 66 KSAIALEMHITYSLIHDDLPAMNDYRSGKLNNHKYVGEMTALLAGDALTLTAFAELIS- 124
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 70 PVACALIMHITYSLIHDDLPAMDNDLRKGPNNHKVFGEMAILLAGDGLLTYAFQILITE 129
QY 125 -SDRLTDEVKIKYLRSLASGHVGVGQMLDMQSEGPIDLETLEMTHKTKTGALLT 183
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAGQAADMEGEGKTLTSLSEYTHRHKTGMLQ 189
QY 184 FAYMSADIANDVDTTKEHLESYSYHIGMMFOIKDILLDCYGEAKLGRKVGSDLENKKS 243
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 190 YSVHAGLIGADARQREIDEPFAHLGLAFQIRDDILIDEGAEKIGKEVGSQSNKKA 249
QY 244 TYVSLGKQGAEDKLTYYHRDAVDELTOID 273
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 250 TYPALSLAGAKKELAFHIAQRLRNAD 279

```

```

RESULT 11
US-09-367-528A-1
/ Sequence 1, Application US/09367528A
/ Patent No. 6395525
/ GENERAL INFORMATION:
/ APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
/ TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
/ FILE REFERENCE: PH-586
/ CURRENT APPLICATION NUMBER: US/09/367,528A
/ PRIOR FILING DATE: 1999-08-16
/ PRIOR APPLICATION NUMBER: JP97/346686
/ PRIOR FILING DATE: 1997-12-16
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 297
/ TYPE: PRT
/ ORGANISM: Bacillus stearothermophilus
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: 82
/ OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,
/ OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, His or Pro.
/ US-09-367-528A-1

```

```

Query Match      44.5%; Score 646; DB 4; Length 297;
Best Local Similarity 49.3%; Pred. No. 3.3e-56;
Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;

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QY 6 MNLKLIDEVNNELSVAINKSVMDTQLEBSMKYSINAGGKRIRPVLLLTLDLSLNTVEYELGM 65
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 10 LNEQKQAVETALSRYSIERLEGPAKKKAAVSLGAGKRIRPVLLLTSTVRLGKDPVAVGL 69
QY 66 KSAIALEMHITYSLIHDDLPAMNDYRSGKLNNHKYVGEMTALLAGDALTLTAFAELIS- 124
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 70 PVACALIMHITYSLIHDDLPAMDNDLRKGPNNHKVFGEMAILLAGDGLLTYAFQILITE 129
QY 125 -SDRLTDEVKIKYLRSLASGHVGVGQMLDMQSEGPIDLETLEMTHKTKTGALLT 183
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAGQAADMEGEGKTLTSLSEYTHRHKTGMLQ 189

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QY 184 FAVMSADIANDVDTTKEHLESYHLMGMFOIKDILLDCYGEAKLGRKVSLENNKS 243
DB 190 YSVHAGALIGGADARQTRLEDEFAHGLAFQIRDDILIDIEGAEEKIGKVPVSDOSNNKA 249
QY 244 TVVSLGKGADKLTYYRDAVDELTOID 273
DB 250 TVPALISLAGAKKLAFFHIEAQRHLRNAD 279

RESULT 12
US-08-534-910B-6
Sequence 6, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: Koyama, Taneoshi
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Ther
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofteneetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-6

Query Match 44.4%; Score 645; DB 1; Length 297;
Best Local Similarity 48.0%; Pred. No. 4,2e-56;
Matches 130; Conservative 56; Mismatches 79; Indels 6; Gaps 2;

QY 1 MTNLPMTKLIDEVNNELSVAINKSVM----DTQLEBSMTVSLNAGGRIRPVLLLTLDLS 56
DB 1 MAQSLVEFLENGQAVETALSRYTEIRLEGPALKKKMAVSLLEGGRIRPFLLSLVRA 60
QY 57 INTEVELGKSAIALEMHTYSLIHDDLPAMDNDYRGRKLTNNKYGEWTAILAGDAL 116
DB 61 LGKPAVGLPVACALIEHTHTSLIHDDLPAMDNDLARGKRTNNKYVGEAMAILAGDGL 120
QY 117 TKAFELIS--SDDRILTDEVKIKVTLORLSIASGHVGMVGOMLDMQSGQPIDETLEMIR 174

DB 121 TYAFQLTIDEIDELIPPSVRRLIERLAKAAGPBGVAGQADWEGKTLTSELSEYIH 180
QY 175 KYTGALITFAVMSADIANDVDTTKEHLESYHLMGMFOIKDILLDCYGEAKLGRKV 234
DB 181 RHKTGKMLQYSVHAGALIGGADARQTRLEDEFAHGLAFQIRDDILIDIEGAEEKIGKPV 240
QY 235 GSDLENNKSTYVSLGKGADKLTYYRDA 265
DB 241 GSDOSNNKATTPALISLAGAKKLAFFHIEA 271

RESULT 13
US-09-367-528A-3
Sequence 3, Application US/09367528A
Patent No. 6395525
GENERAL INFORMATION:
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
FILE REFERENCE: PH-586
CURRENT APPLICATION NUMBER: US/09/367,528A
PRIOR FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: JP97/346686
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-367-528A-3

Query Match 44.3%; Score 644; DB 4; Length 297;
Best Local Similarity 49.3%; Pred. No. 5.3e-56;
Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;

QY 6 MNKLTIDEVNNELSVAINKSVMDTQLEBSMTVSLNAGGRIRPVLLLTLDLSINTEYELGM 65
DB 10 LNEGQAVETALSRYTEIRLEGPALKKKMAVSLLEGGRIRPFLLSLVRAVG 69
QY 66 KSAIALEMIHTYSLIHDDLPAMDNDYRGRKLTNNKYGEWTAILAGDALITKAFELIS- 124
DB 70 PVACALIEHTHTYFLIHDDLPAMDNDLARGKRTNNKYVGEAMAILAGDGLTYAFQLTITE 129
QY 125 -SDDRILTDEVKIKVTLORLSIASGHVGMVGOMLDMQSGQPIDETLEMIRKTKGALLT 183
DB 130 IDDERIPPSVRRLIERLAKAAGPBGVAGQADWEGKTLTSELSEYIRHKTGKMLQ 189
QY 184 FAVMSADIANDVDTTKEHLESYHLMGMFOIKDILLDCYGEAKLGRKVSLENNKS 243
DB 190 YSVHAGALIGGADARQTRLEDEFAHGLAFQIRDDILIDIEGAEEKIGKVPVSDOSNNKA 249
QY 244 TVVSLGKGADKLTYYRDAVDELTOID 273
DB 250 TVPALISLAGAKKLAFFHIEAQRHLRNAD 279

RESULT 14
US-09-275-742-2
Sequence 2, Application US/09275742
Patent No. 6130069
GENERAL INFORMATION:
APPLICANT: Wilding, Edwin Michael
APPLICANT: Gwynn, Michael
TITLE OF INVENTION: 18PA
FILE REFERENCE: GM10205
CURRENT APPLICATION NUMBER: US/09/275,742
CURRENT FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT

Page 7

ORGANISM: Enterococcus faecium

Qy	13	VNNLESLVANKSMVDTOLJESMLTSLYNGRRIRIPVLLLTJDSLNTYEYKGM-KSIAL	71
Db	30	VEKEISLFPDEHTTTRGVLTDAMSYSVKAGGRIRIPVLLLTJDSLNTYEYKGM-FDEPRIDIVPVQVAAAL	69
Qy	72	EMHTVSLIHDDLPAMDNDPYRGCTTHKKYVGEWTAIIAGDALLTFAFELISGDRPLTD	131
Db	90	EMWHTSLIHDDLPAMDNDLRRGKPTTHKKYFGEALTAIAGDGLLTGAFOLISW-AHIGN	148
Qy	132	EYVIKYLQGLTSLASHGVGVGGWMDMOSEOPDLFTLEWTHHKTKGALLTFVPMASAD	191
Db	149	SPTGLLIHQGLAVCAGSGGVVAGQADIGESKCLSTBELAVTHERKQGHILRYALLAGGI	208
Qy	192	IANDVDTTKEHLESTYHLSGMFFQYKDDLLCYGDEAKLGGKVSQSLNNKSTVYSLLGK	251
Db	209	LAQPSRSLIILQLRLSHLGGALFQIRDDLLVIGTTKLGKTAGKDERMEKNTYPRLLGL	268
Qy	252	DGAEDKLTYNRDAVDELTDIDE	274
Db	269	EKTRALEIEILLANKKIDKLEE	291

Search completed: April 19, 2004, 15:49:32
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2004, 15:48:07 ; Search time 47 seconds

(without alignments)
1683.366 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 1453
Sequence: 1 MTNLLPMNKLIDEVNNELSLVA.....ELTQIDCEQNTKHLLEIVDL 287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1124875 segs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1453	100.0	287	9	US-09-925-637-64
2	1453	100.0	287	14	US-10-084-205-64
3	1444	99.4	293	12	US-10-282-122A-44363
4	1442	99.2	293	9	US-09-815-242-12583
5	1415	97.4	288	9	US-09-815-242-5239
6	1040	71.6	293	12	US-10-282-122A-71252
7	1015	69.9	293	12	US-10-282-122A-70715
8	702.5	48.3	293	12	US-10-282-122A-60940
9	650	44.7	297	12	US-10-462-698A-76
10	638	43.9	294	15	US-10-369-493-17358
11	636.5	43.8	272	15	US-10-369-493-23301
12	617	42.5	297	15	US-10-369-493-16549
13	615	42.3	296	12	US-10-282-122A-45490
14	596	41.0	293	9	US-09-815-242-10630
15	596	41.0	293	12	US-10-282-122A-57289

16	578.5	39.8	261	15	US-10-369-493-9710	Sequence 9710, Ap
17	568	39.1	295	12	US-10-282-122A-53246	Sequence 53246, A
18	557	38.3	294	12	US-10-282-122A-52706	Sequence 52706, A
19	556	38.1	290	15	US-10-369-493-20893	Sequence 20893, A
20	554	38.1	289	12	US-10-282-122A-72262	Sequence 72262, A
21	551.5	38.0	290	12	US-10-282-122A-74642	Sequence 74642, A
22	549	37.8	291	9	US-09-815-242-13597	Sequence 13597, A
23	547	37.6	291	9	US-09-815-242-13273	Sequence 13273, A
24	547	37.6	291	12	US-10-282-122A-73998	Sequence 73998, A
25	544.5	37.5	310	15	US-10-369-493-19922	Sequence 19922, A
26	541.5	37.3	265	12	US-10-282-122A-57443	Sequence 57443, A
27	540.5	37.2	285	15	US-10-369-493-18391	Sequence 18391, A
28	534.5	36.8	309	15	US-10-369-493-18752	Sequence 18752, A
29	532	36.6	289	12	US-10-282-122A-51526	Sequence 51526, A
30	526.5	36.2	302	15	US-10-369-493-2608	Sequence 2608, Ap
31	524	36.1	291	15	US-10-369-493-8506	Sequence 8506, Ap
32	516.5	35.5	297	9	US-09-934-903-14	Sequence 14, Appl
33	516.5	35.5	297	9	US-09-934-868-72	Sequence 72, Appl
34	516.5	35.5	297	10	US-09-941-947A-20	Sequence 20, Appl
35	516.5	35.5	297	12	US-10-700-003-14	Sequence 14, Appl
36	515.5	35.5	306	15	US-10-369-493-10187	Sequence 10187, A
37	504.5	34.7	367	13	US-10-108-915-26	Sequence 26, Appl
38	497.5	34.2	295	9	US-09-815-242-11239	Sequence 11239, A
39	497.5	34.2	295	12	US-10-282-122A-58515	Sequence 58515, A
40	495.5	34.1	296	15	US-10-369-493-21173	Sequence 21173, A
41	495.5	34.1	350	12	US-10-424-599-268482	Sequence 268482, A
42	494.5	34.0	353	12	US-10-425-114-47693	Sequence 47693, A
43	494.5	34.0	350	13	US-10-108-915-22	Sequence 22, Appl
44	492.5	33.9	268	12	US-10-282-122A-45768	Sequence 45768, A
45	492	33.9	287	15	US-10-369-493-19191	Sequence 19191, A

ALIGNMENTS

RESULT 1
US-09-925-637-64
Sequence 64, Application US/09925637
Patent No. US2002010338A1
GENERAL INFORMATION:
APPLICANT: Chou
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: P8560
CURRENT APPLICATION NUMBER: US/09/925.637
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/151,933
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781,986
PRIOR FILING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 287
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-637-64
Query Match 100.0%; Score 1453; DB 9; Length 287;
Best local similarity 100.0%; Pred. No. 4.6e-139; Indels 0; Gaps 0;
Matches 287; Conservative 0;
QY 1 MTNLPNKLIDEVNNELSLVA...INKSYMDTQLESMLYSINAGGKIRIPVLLLTDSINTE 60
Db 1 MTNLPNKLIDEVNNELSLVA...INKSYMDTQLESMLYSINAGGKIRIPVLLLTDSINTE 60
QY 61 YELGKSAIALEMHTTSLIHDDLPAMNDYDRGKLTNHRVYGEWTAIAGDALLTKAF 120

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Db      61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIILAGDALLTKAF 120
QY      121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
        121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
QY      181 LITPAVMSADIANVDDTTKEHLESYSYHLGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240
        181 LITPAVMSADIANVDDTTKEHLESYSYHLGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240
Db      241 NKSTYVSLGKGGAEDKLTYHRDAVDELTOIDEQFNTKHLLEIVDL 287
        241 NKSTYVSLGKGGAEDKLTYHRDAVDELTOIDEQFNTKHLLEIVDL 287

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RESULT 2

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US-10-084-205-64
; Sequence 64, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, GJ1
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P851P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 64
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-084-205-64

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Query Match      100.0%; Score 1453; DB 14; Length 287;
Best Local Similarity 100.0%; Pred. No. 4,6e-139;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        1 MTNLPNKLIDEVNNELSVAINKSYMDTOLESMLYSINAGKRIKRPVLLLTDSLNT 60
Db      61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIILAGDALLTKAF 120
        61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIILAGDALLTKAF 120
QY      121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
        121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
Db      121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
        121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
QY      181 LITPAVMSADIANVDDTTKEHLESYSYHLGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240
        181 LITPAVMSADIANVDDTTKEHLESYSYHLGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240
Db      241 NKSTYVSLGKGGAEDKLTYHRDAVDELTOIDEQFNTKHLLEIVDL 287
        241 NKSTYVSLGKGGAEDKLTYHRDAVDELTOIDEQFNTKHLLEIVDL 287

```

RESULT 3

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US-10-282-122A-44363
; Sequence 44363, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith

```

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; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44363
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-44363

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Query Match      99.4%; Score 1444; DB 12; Length 293;
Best Local Similarity 99.3%; Pred. No. 3,9e-138;
Matches 285; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MTNLPNKLIDEVNNELSVAINKSYMDTOLESMLYSINAGKRIKRPVLLLTDSLNT 60
        1 MTNLPNKLIDEVNNELSVAINKSYMDTOLESMLYSINAGKRIKRPVLLLTDSLNT 60
Db      61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIILAGDALLTKAF 120
        61 YELGKSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKVGEMTAIILAGDALLTKAF 120
QY      121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
        121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
Db      121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
        121 ELISSDRRLTDEVKIKYLOSLIASGHVGVGGMLDMOSEGQPIDLETLEMHKTKTGA 180
QY      181 LITPAVMSADIANVDDTTKEHLESYSYHLGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240
        181 LITPAVMSADIANVDDTTKEHLESYSYHLGMMFQIKODLLDCYDGEAKLGGKVGSDLEN 240
Db      241 NKSTYVSLGKGGAEDKLTYHRDAVDELTOIDEQFNTKHLLEIVDL 287
        241 NKSTYVSLGKGGAEDKLTYHRDAVDELTOIDEQFNTKHLLEIVDL 287

```

RESULT 4

```

US-09-815-242-12583
; Sequence 12583, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel

```

```
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12583
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-815-242-12583

Query Match          99.3%; Score 1442; DB 9; Length 293;
Best Local Similarity 99.3%; Pred. No. 6,2e-138;
Matches 285; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTNLPNKLIDEVNNELSAVINKSVMDTQLESMLYSINAGGRIRPVLLLTDSINTFELGM 60
DB 1 MTNLPNKLIDEVNNELSAVINKSVMDTQLESMLYSINAGGRIRPVLLLTDSINTFELGM 60
QY 61 YELGMSALALEMITHYSLIHDDLPMNDNDYRGLTNHKYGEWTAIIAGDALLTKAF 120
DB 61 YELGMSALALEMITHYSLIHDDLPMNDNDYRGLTNHKYGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEYKIKVRLSLASGHVGVGQMLDMSQPIDLETLEMHKTGTGA 180
DB 121 ELISSDRLTDEYKIKVRLSLASGHVGVGQMLDMSQPIDLETLEMHKTGTGA 180
QY 181 LITFAVMSAADIANVDTKHELESYSHLGMMFOIKDILLDCYGEAKLGKVGSDLEN 240
DB 181 LITFAVMSAADIANVDTKHELESYSHLGMMFOIKDILLDCYGEAKLGKVGSDLEN 240
QY 241 NKSTVYSLGKDAEDKLTYHRDAVDELTOIDEQNTKHLLEIVDL 287
DB 241 NKSTVYSLGKDAEDKLTYHRDAVDELTOIDEQNTKHLLEIVDL 287

RESULT 5
US-09-815-242-5239
/ Sequence 5239, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
```

```
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5239
/ LENGTH: 288
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-815-242-5239

Query Match          97.4%; Score 1415; DB 9; Length 288;
Best Local Similarity 99.3%; Pred. No. 3.4e-135;
Matches 280; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 MKKLIDEVNNELSAVINKSVMDTQLESMLYSINAGGRIRPVLLLTDSINTFELGM 65
DB 1 MKKLIDEVNNELSAVINKSVMDTQLESMLYSINAGGRIRPVLLLTDSINTFELGM 60
QY 66 KSAIAlEMITHYSLIHDDLPMNDNDYRGLTNHKYGEWTAIIAGDALLTKAFELISS 125
DB 61 KSAIAlEMITHYSLIHDDLPMNDNDYRGLTNHKYGEWTAIIAGDALLTKAFELISS 120
QY 126 DDLRLTDEYKIKVRLSLASGHVGVGQMLDMSQPIDLETLEMHKTGTGALLTFA 185
DB 121 DDLRLTDEYKIKVRLSLASGHVGVGQMLDMSQPIDLETLEMHKTGTGALLTFA 180
QY 186 VMSAADIANVDTKHELESYSHLGMMFOIKDILLDCYGEAKLGKVGSDLENNKSTY 245
DB 181 VMSAADIANVDTKHELESYSHLGMMFOIKDILLDCYGEAKLGKVGSDLENNKSTY 240
QY 246 VSLGKDAEDKLTYHRDAVDELTOIDEQNTKHLLEIVDL 287
DB 241 VSLGKDAEDKLTYHRDAVDELTOIDEQNTKHLLEIVDL 282

RESULT 6
US-10-282-122A-71252
/ Sequence 71252, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
```

```

; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 71252
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71252
```

Query Match 71.6%; Score 1040; DB 12; Length 293;

Best Local Similarity 69.0%; Pred. No. 4.5e-97; Mismatches 47; Indels 0; Gaps 0;

Matches 198; Conservative 42; Mismatches 47; Indels 0; Gaps 0;

```

QY 1 MTNLPNKLIDVNNELSVAINKSVMDQLEBSMLYSNAGKRIKRPVLLITLDSLNT 60
DB 1 MAKSMANLINOISALGCVETSPINTNLESQYSLNAGKRIKRPVLLITLDSLNT 60
QY 61 YELGKSAIALEMIHYSILIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
DB 61 YKKGKTAIALEMIHYSILIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
QY 121 ELISDDRLTDEVKIKVLRSLASGHVGMVGOMLDMOSGCPIDLETLMIHKTGA 180
DB 121 ELIADDELLESVKKILSRLANSGHVGQGLDMOSGCPIDLETLMIHKTGA 180
QY 121 ELIADDELLESVKKILSRLANSGHVGQGLDMOSGCPIDLETLMIHKTGA 180
DB 121 ELIADDELLESVKKILSRLANSGHVGQGLDMOSGCPIDLETLMIHKTGA 180
QY 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
DB 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
QY 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
DB 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
QY 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
QY 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287

RESULT 7
US-10-282-122A-70715
; Sequence 70715, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
```

```

; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 70715
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70715
```

Query Match 69.9%; Score 1015; DB 12; Length 293;

Best Local Similarity 68.6%; Pred. No. 1.6e-94; Mismatches 49; Indels 0; Gaps 0;

Matches 197; Conservative 41; Mismatches 49; Indels 0; Gaps 0;

```

QY 1 MTNLPNKLIDVNNELSVAINKSVMDQLEBSMLYSNAGKRIKRPVLLITLDSLNT 60
DB 1 MKKQNNKLINILINSLSNLSOSSPLKTNLESMTKSLNAGKRIKRPVLLITLDSLNT 60
QY 61 YELGKSAIALEMIHYSILIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
DB 61 YQGGNSALALAMIHYSILIHDDLPAMNDYRRGKLTNNKVGEMWTAIIAGDALLTKAF 120
QY 121 ELISDDRLTDEVKIKVLRSLASGHVGMVGOMLDMOSGCPIDLETLMIHKTGA 180
DB 121 ELISDDRLTDEVKIKVLRSLASGHVGMVGOMLDMOSGCPIDLETLMIHKTGA 180
QY 121 ELISDDRLTDEVKIKVLRSLASGHVGMVGOMLDMOSGCPIDLETLMIHKTGA 180
DB 121 ELISDDRLTDEVKIKVLRSLASGHVGMVGOMLDMOSGCPIDLETLMIHKTGA 180
QY 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
DB 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
QY 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
DB 181 LITFAVMSAADIANVDITKEHLESYHLGMMFQIKDLDLCYGEAKLGKVGSDLEN 240
QY 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
QY 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
DB 241 NKSTYVSLIGKGAEDKLTYHRDAVDELTOIDQFNTKHLLEIVDL 287
```

RESULT 8

US-10-282-122A-60940

; Sequence 60940, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyckind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; PRIOR FILING DATE: 2003-02-20


```

RESULT 11
US-10-369-493-23201
; Sequence 23201, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23201
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23201

```

```

Query Match      43.8%; Score 636.5; DB 15; Length 272;
Best Local Similarity 49.3%; Pred. No. 4,1e-56;
Matches 134; Conservative 51; Mismatches 82; Indels 5; Gaps 2;

```

```

QY 1 MTNLPNKLIDE--VNNELSYAINKSVYDTQLESMLSYLNAGKIRPVLLLTLDL 57
DB 1 MTNKLTSFLADRKRTIENQSLSYTEKLMPSLKKSMYSIQAGGKRLRPLIVAVANAY 60
QY 58 NTEVYELKMSAIALEMITYSLIHDDLPAMDNDYRKKLTNHYVGEWTAIAGDALLT 117
DB 61 GKSEKDGIPVGCVAEMHTYSLIHDDLPAMDNDYRKKLTNHYVGEWTAIAGDALLT 120
QY 118 KAFELISS--DDRLEDEYKIVLQRLSIASGVGVGGQMLDNOSQGPIDLETLEMTHK 175
DB 121 ESFKLITHVSDVEVAERKLRLVNELISAAGTEGVGVQVADMAAGRQVTLLESLIHE 180
QY 176 TTTGALLTPAAMSADIANVDPTTEHLESYSYHGMFFQIKDLDYCGEALGKVG 235
DB 181 RTSKLIFGVYAGAILDAPEEDITLRTSSHIGIFQIRDDILDESGSEKIGKVG 240
QY 236 SDLENNKSTVYSLGKDAQEDKLTYHRDAVD 267
DB 241 SPTTNDKSTYPSLBSLEGAKHLDVHIKEAND 272

```

```

RESULT 12
US-10-369-493-16549
; Sequence 16549, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16549
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

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US-10-369-493-16549

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```

Query Match      42.5%; Score 617; DB 15; Length 297;
Best Local Similarity 46.6%; Pred. No. 4,5e-54;
Matches 129; Conservative 57; Mismatches 87; Indels 4; Gaps 2;

```

```

QY 13 VNNELSYAINKSVYDTQLESMLSYLNAGKIRPVLLLTLDLNTLEYELKMSAIAE 72
DB 17 VEKLVSYNELQCPNVLEAAYSLDEGKRLRPFLPAIQARKENLVGAACAE 76
QY 73 MHTYSLIHDDLPAMDNDYRKKLTNHYVGEWTAIAGDALLTKAFELISSDR--LT 130
DB 77 MHTYSLVHDDLPAMDNDYRKKLTNHYVGEWTAIAGDALLTKAFELISSDR--LT 136
QY 131 DEKIVLVORLSIASGVGVGGQMLDNOSQGPIDLETLEMTHKTKGALLTPAAMSAA 190
DB 137 AERKVLVLELAKAAGPEGMVGVQVADMAEGRKLTLELYIHKTKGLLEPAVLAA 196
QY 191 DIANVDPTTEHLESYSYHGMFFQIKDLDYCGEALGKVGSDLENNKSTVYSLIG 250
DB 197 IISDATEBOEKLTLPKAKIGLAFQIRDDILDESGSEKIGKISDSLEKSTYTLPT 256
QY 251 KQGAEDKLTYHRDAVDLTQIDEPNTKHLLEIVDL 287
DB 257 VDRKDILETETIAEAKGAISL--QLODEYLLSIDL 291

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```

RESULT 13
US-10-282-122A-45490
; Sequence 45490, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45490
; LENGTH: 296

```

TYPE: PRT
ORGANISM: Bacillus anthracis
US-10-282-122A-45490

Query Match 42.3%; Score 615; DB 12; Length 296;
Best Local Similarity 46.2%; Pred. No. 7,1e-54;
Matches 128; Conservative 56; Mismatches 89; Indels 4; Gaps 2;

QY 13 VNNEISVAINKSVMDTOEESMTLSINAGKRIRPVLLLTLDLNTNEYELGMSATALE 72
DB 16 VEEKVASANEQCPNIREANVSLENGKRLPLFPATLOAPDERNLGVGAACALE 75
QY 73 MIHTYSLIHDDLPMANDDYRGRKLTNNKYGWETAILIAGDALITKAFELISS--DDRLT 130
DB 76 MIHTYSLVHDDLPCMDDDDLRGRKPTNKKVFGEMAAVLADGGLLTFAFOVIMAYGQKEIS 135
QY 131 DEVKIKVLOSLASGHVGMVGQMLDMOSGQPIDLETLEMINKTKTGALLTFAVMSAA 190
DB 136 AEKRVLYLEAKAGPBGWGGVADAEAGKOLTTIDLEYIKHKTKGKLEPAVLAGS 195
QY 191 DIANVDTTKEHLESYSYHLGMMFOIKDLDLCYDGEAKLGKVGSDLENKSKTYVSILG 250
DB 196 ILSDAETGEQELLPFAKYGAFIRDDIDVETGEIEIKRPIGSDVSNKSTYTTLLFT 255
QY 251 KDGAEKLTTHRDAVDELTOIDEGFNTKHLLEIVDL 287
DB 256 VDRADIDLETAKAKDAIGSL--QLDEVELLSICDL 290

RESULT 14

US-09-815-242-10630
Sequence 10630, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10630
LENGTH: 293
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-815-242-10630

Query Match 41.0%; Score 596; DB 9; Length 293;
Best Local Similarity 46.0%; Pred. No. 5.9e-52;
Matches 134; Conservative 56; Mismatches 91; Indels 10; Gaps 5;

QY 1 MTNLPMN--KLIDEVNNEISVAINKSVMDTOEESMTLSINAGKRIRPVLLLTLDLSIN 58
DB 1 MTNFSQCHLPVEKRWVDF---IAETNERLEKNELVSIHNGGRRLRLVLVTTAAAG 57
QY 59 TEYEL-GMSAIALEMIHTYSLIHDDLPMANDDYRGRKLTNNKYGWETAILIAGDALIT 117
DB 58 KEMETODCVVAASTLEMIHTYSLIHDDLPMADDLDRGRKPTNKKVFGAETAILIAGDGLT 117
QY 118 KAPELSSDRLTDEVKIKVLOSLASGHVGMVGQMLDMOSGQPIDLETLEMINKTK 177
DB 118 GAFQSLSLSQLGISE-KVLMQQLATAAGNQGVMGDIEGKYSITLBEIAVAHEKK 176
QY 178 TGAULTFAVMSAADIANVDTTKEHLESYSYHLGMMFOIKDLDLCYDGEAKLGKVGSD 237
DB 177 TGALEFALIAAGVLANQTEEVIGLLTFPAHHYGLAFQIRDDLLDATSTEADLGKVGSD 236
QY 238 LENNKSTYVSILGKDGAEKLTTH--HRDAVDELTOIDEGFNTKHLLEIV 285
DB 237 EALNKSTYPALGIGAGAKDALTTHQLAEGSAVLEKTAANPNSEBHLANIL 287

RESULT 15

US-10-282-122A-57289
Sequence 57289, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57289
LENGTH: 293
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-10-282-122A-57289

Query Match 41.0%; Score 596; DB 12; Length 293;
Best Local Similarity 46.0%; Pred. No. 5.9e-52;

Tue Apr 20 12:43:41 2004

us-09-925-637-64_1.rapb

Page 8

	Matches	134;	Conservative	56;	Mismatches	91;	Indels	10;	Gaps	5;
QY	1	MTYLPWN--KLIDVNNNELSVAINKSVMDTQLESMLYSLNAGGKRIKRPVLLLLTIDSLN	58							
Db	1	MINFSQOHLPLVEKVVDF--IAEYTERERLKEAMLYSIHAGGKRLRPLLVLTVAAFQ	57							
QY	59	TEYEL-GMKSAIALEMHTYSLIHDDLPAAMDNDYRGRKLTNNKXYGEWTAIAGDALIT	117							
Db	58	KEMETQDYVAASLEMIHTYSLIHDDLPAAMDDDLARGKPTNKKVFGAATAIAGDGLT	117							
QY	118	KAFELISSDRRLTDEYKIKVLQRLSTASGHVGVGGQMLDMQSEGQPIDLETLEMHKTK	177							
Db	118	GAFQLSLSQLSE-KVLLMOQLAKAAGNQGMSGMDIBGEKVSITLBEIAAVHERK	176							
QY	178	TGALLTFAVMSADIANDVDTTKEHLESYSYHLGMMFOIKDDLLDCYGDPAKLGKKVGS	237							
Db	177	TGALLIEFALTAGVLANQTEVIGLLTQFAHHYGLAFQIRDDLLDATSTEADLGKKVGR	236							
QY	238	LENNKSTYVSLGKDGAEKLY--HRDAVDELQIDQFNTKHLLEIV	285							
Db	237	EALNKSTYFALGLIAGAKDALTHQLAEGSAVLEKIKANVPNFSEHLANIL	287							

Search completed: April 19, 2004, 15:54:17
Job time : 48 secs